

SEARCH REQUEST FORM

7.511

Requestor's Name: Nancy Johnson Serial Number: 091047,652
Date: 7-20-98 Phone: 305-5860 Art Unit: 1642

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

Please search SEQ ID NO:1-3

Please do an interference search of

Seq ID NO:1-3.

Return on paper print out.

Thanks!

Nancy J.

1998 JUL 20 PM 3:29

STAFF USE ONLY

Date completed: 7/22/98
Searcher: Sheppard
Terminal time: _____
Elapsed time: _____
CPU time: _____
Total time: _____
Number of Searches: _____
Number of Databases: _____

Search Site
_____ STIC
_____ CM-1
_____ Pre-S
Type of Search
_____ N.A. Sequence
_____ A.A. Sequence
_____ Structure
_____ Bibliographic

Vendors
_____ IG Suite
_____ STN
_____ Dialog
_____ APS
_____ Geninfo
_____ SDC
_____ DARC/Questel
_____ Other

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[W][A][T][E][R][M][A][N]
[S][E][Q][U][E][N][C][E]
[A][L][I][G][N][M][E][N][T]
[P][R][O][G][R][A][M]
(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Tue Jul 21 14:53:17 1998; MasPar time 828.83 Seconds
Tabular output not generated.
1312.667 Million cell updates/sec

Title: >US-09-047-652A-1
Description: (1-652) from US09047652A.seq
Perfect Score: 652
N.A. Sequence: 1 CCACGGCGAAGTCTCGCT.....GTTCTTGGACATGGAATTT 652
Comp: GGTGCGGCTTCAGAGCGA.....CAAGAACCTTGACCTTAA

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0
Searched: 457396 seqs, 834342348 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: emb154
1:em_ba 2:em_htg 3:em_hum1 4:em_hum2 5:em_in 6:em_om
7:em_or 8:em_lov 9:em_pat 10:em_pl 11:em_ro 12:em_v1
Database: genbank106
13:gb_ba 14:gb_htg 15:gb_in 16:gb_om 17:gb_ov 18:gb_pat
19:gb_pl 20:gb_pl 21:gb_pr1 22:gb_pr2 23:gb_ro 24:gb_st
25:gb_sy 26:gb_un 27:gb_v1
Statistics: Mean 10.377; Variance 5.497; scale 1.888

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES							
Result No.	Score	Query Match	Length	ID	Description	Pred. No.	
1	643	98.6	821	21	HUMHPBS	Human peripheral benzo	0.00e+00
2	542	83.1	639	21	HUMBENZA	Human peripheral benzo	0.00e+00
3	403	61.8	684	21	HSPBR4	Human peripheral benzo	3.85e-288
4	403	61.8	160559	14	HS1191B2	Human DNA sequence ***	3.85e-288
5	402	61.7	4258	21	HSU12421	Human mitochondrial be	2.43e-287
6	384	58.9	152843	14	HS526114	Human DNA sequence ***	5.93e-273
7	288	44.2	821	16	BOVPBRIBP	Calf peripheral-type b	1.44e-196
8	282	43.3	626	23	MUSMPBR	Mouse peripheral-type	8.06e-192
9	276	42.3	781	23	RATPKBSX	Rat peripheral-type be	4.49e-187
10	274	42.0	856	23	MUSPTBR	Mouse mRNA for periphe	1.71e-185
11	128	19.6	645	21	HSPBR3	Human peripheral benzo	6.34e-72
12	115	17.6	3434	23	RATPTBRZ02	Rat peripheral-type be	3.97e-62
13	106	16.3	487	21	HSPBR2	Human peripheral benzo	2.10e-55
14	39	6.0	7218	18	I66494	Sequence 14 from paten	1.82e-08
15	37	5.7	1084	23	CGU12420	Cricetulus griseus mit	3.04e-07

Sequence 5 from patent									
1.22e-06	1.22e-06	1.22e-06	1.22e-06	1.22e-06	1.22e-06	1.22e-06	1.22e-06	1.22e-06	1.22e-06
Mus musculus mitochond	Mus musculus mitochond	Mus musculus mitochond	Mus musculus mitochond	Mus musculus mitochond	Mus musculus mitochond	Mus musculus mitochond	Mus musculus mitochond	Mus musculus mitochond	Mus musculus mitochond
Sequence 5 from patent	Sequence 5 from patent	Sequence 5 from patent	Sequence 5 from patent	Sequence 5 from patent	Sequence 5 from patent	Sequence 5 from patent	Sequence 5 from patent	Sequence 5 from patent	Sequence 5 from patent
carotenoid gene cluste	carotenoid gene cluste	carotenoid gene cluste	carotenoid gene cluste	carotenoid gene cluste	carotenoid gene cluste	carotenoid gene cluste	carotenoid gene cluste	carotenoid gene cluste	carotenoid gene cluste
R.sphaeroides crt gene	R.sphaeroides crt gene	R.sphaeroides crt gene	R.sphaeroides crt gene	R.sphaeroides crt gene	R.sphaeroides crt gene	R.sphaeroides crt gene	R.sphaeroides crt gene	R.sphaeroides crt gene	R.sphaeroides crt gene
gDNA encoding envelope	gDNA encoding envelope	gDNA encoding envelope	gDNA encoding envelope	gDNA encoding envelope	gDNA encoding envelope	gDNA encoding envelope	gDNA encoding envelope	gDNA encoding envelope	gDNA encoding envelope
Homo sapiens calcium-a	Homo sapiens calcium-a	Homo sapiens calcium-a	Homo sapiens calcium-a	Homo sapiens calcium-a	Homo sapiens calcium-a	Homo sapiens calcium-a	Homo sapiens calcium-a	Homo sapiens calcium-a	Homo sapiens calcium-a
Homo sapiens intermed	Homo sapiens intermed	Homo sapiens intermed	Homo sapiens intermed	Homo sapiens intermed	Homo sapiens intermed	Homo sapiens intermed	Homo sapiens intermed	Homo sapiens intermed	Homo sapiens intermed
A.hydrophila amonabact	A.hydrophila amonabact	A.hydrophila amonabact	A.hydrophila amonabact	A.hydrophila amonabact	A.hydrophila amonabact	A.hydrophila amonabact	A.hydrophila amonabact	A.hydrophila amonabact	A.hydrophila amonabact
Human tristetrapollin	Human tristetrapollin	Human tristetrapollin	Human tristetrapollin	Human tristetrapollin	Human tristetrapollin	Human tristetrapollin	Human tristetrapollin	Human tristetrapollin	Human tristetrapollin
H.sapiens zinc finger	H.sapiens zinc finger	H.sapiens zinc finger	H.sapiens zinc finger	H.sapiens zinc finger	H.sapiens zinc finger	H.sapiens zinc finger	H.sapiens zinc finger	H.sapiens zinc finger	H.sapiens zinc finger
Homo sapiens intermed	Homo sapiens intermed	Homo sapiens intermed	Homo sapiens intermed	Homo sapiens intermed	Homo sapiens intermed	Homo sapiens intermed	Homo sapiens intermed	Homo sapiens intermed	Homo sapiens intermed
Homo sapiens intermed	Homo sapiens intermed	Homo sapiens intermed	Homo sapiens intermed	Homo sapiens intermed	Homo sapiens intermed	Homo sapiens intermed	Homo sapiens intermed	Homo sapiens intermed	Homo sapiens intermed
Homo sapiens zinc fing	Homo sapiens zinc fing	Homo sapiens zinc fing	Homo sapiens zinc fing	Homo sapiens zinc fing	Homo sapiens zinc fing	Homo sapiens zinc fing	Homo sapiens zinc fing	Homo sapiens zinc fing	Homo sapiens zinc fing
Mycobacterium smegmati	Mycobacterium smegmati	Mycobacterium smegmati	Mycobacterium smegmati	Mycobacterium smegmati	Mycobacterium smegmati	Mycobacterium smegmati	Mycobacterium smegmati	Mycobacterium smegmati	Mycobacterium smegmati
5.42e+00	5.42e+00	5.42e+00	5.42e+00	5.42e+00	5.42e+00	5.42e+00	5.42e+00	5.42e+00	5.42e+00
Homo sapiens WSCR4 gen	Homo sapiens WSCR4 gen	Homo sapiens WSCR4 gen	Homo sapiens WSCR4 gen	Homo sapiens WSCR4 gen	Homo sapiens WSCR4 gen	Homo sapiens WSCR4 gen	Homo sapiens WSCR4 gen	Homo sapiens WSCR4 gen	Homo sapiens WSCR4 gen
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ntfB, ntrC [Azospirilli	ntfB, ntrC [Azospirilli	ntfB, ntrC [Azospirilli	ntfB, ntrC [Azospirilli	ntfB, ntrC [Azospirilli	ntfB, ntrC [Azospirilli	ntfB, ntrC [Azospirilli	ntfB, ntrC [Azospirilli	ntfB, ntrC [Azospirilli	ntfB, ntrC [Azospirilli
5.42e+00	5.42e+00	5.42e+00	5.42e+00	5.42e+00	5.42e+00	5.42e+00	5.42e+00	5.42e+00	5.42e+00
Homo sapiens mRNA for	Homo sapiens mRNA for	Homo sapiens mRNA for	Homo sapiens mRNA for	Homo sapiens mRNA for	Homo sapiens mRNA for	Homo sapiens mRNA for	Homo sapiens mRNA for	Homo sapiens mRNA for	Homo sapiens mRNA for
5.42e+00	5.42e+00	5.42e+00	5.42e+00	5.42e+00	5.42e+00	5.42e+00	5.42e+00	5.42e+00	5.42e+00
Rattus norvegicus type	Rattus norvegicus type	Rattus norvegicus type	Rattus norvegicus type	Rattus norvegicus type	Rattus norvegicus type	Rattus norvegicus type	Rattus norvegicus type	Rattus norvegicus type	Rattus norvegicus type
5.42e+00	5.42e+00	5.42e+00	5.42e+00	5.42e+00	5.42e+00	5.42e+00	5.42e+00	5.42e+00	5.42e+00
Mouse opsin (MOPS) gen	Mouse opsin (MOPS) gen	Mouse opsin (MOPS) gen	Mouse opsin (MOPS) gen	Mouse opsin (MOPS) gen	Mouse opsin (MOPS) gen	Mouse opsin (MOPS) gen	Mouse opsin (MOPS) gen	Mouse opsin (MOPS) gen	Mouse opsin (MOPS) gen
5.42e+00	5.42e+00	5.42e+00	5.42e+00	5.42e+00	5.42e+00	5.42e+00	5.42e+00	5.42e+00	5.42e+00
Homo sapiens PAC clone	Homo sapiens PAC clone	Homo sapiens PAC clone	Homo sapiens PAC clone	Homo sapiens PAC clone	Homo sapiens PAC clone	Homo sapiens PAC clone	Homo sapiens PAC clone	Homo sapiens PAC clone	Homo sapiens PAC clone
5.42e+00	5.42e+00	5.42e+00	5.42e+00	5.42e+00	5.42e+00	5.42e+00	5.42e+00	5.42e+00	5.42e+00
Sequence 142 from pate	Sequence 142 from pate	Sequence 142 from pate	Sequence 142 from pate	Sequence 142 from pate	Sequence 142 from pate	Sequence 142 from pate	Sequence 142 from pate	Sequence 142 from pate	Sequence 142 from pate
1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01
Human placental alkali	Human placental alkali	Human placental alkali	Human placental alkali	Human placental alkali	Human placental alkali	Human placental alkali	Human placental alkali	Human placental alkali	Human placental alkali
1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01
Human alkaline phospho	Human alkaline phospho	Human alkaline phospho	Human alkaline phospho	Human alkaline phospho	Human alkaline phospho	Human alkaline phospho	Human alkaline phospho	Human alkaline phospho	Human alkaline phospho
1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01
Human placental alkali	Human placental alkali	Human placental alkali	Human placental alkali	Human placental alkali	Human placental alkali	Human placental alkali	Human placental alkali	Human placental alkali	Human placental alkali
1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01
Cloning vector pSEAP2-	Cloning vector pSEAP2-	Cloning vector pSEAP2-	Cloning vector pSEAP2-	Cloning vector pSEAP2-	Cloning vector pSEAP2-	Cloning vector pSEAP2-	Cloning vector pSEAP2-	Cloning vector pSEAP2-	Cloning vector pSEAP2-
1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01
Rhodobacter capsulatus	Rhodobacter capsulatus	Rhodobacter capsulatus	Rhodobacter capsulatus	Rhodobacter capsulatus	Rhodobacter capsulatus	Rhodobacter capsulatus	Rhodobacter capsulatus	Rhodobacter capsulatus	Rhodobacter capsulatus
1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01
Homo sapiens chromosom	Homo sapiens chromosom	Homo sapiens chromosom	Homo sapiens chromosom	Homo sapiens chromosom	Homo sapiens chromosom	Homo sapiens chromosom	Homo sapiens chromosom	Homo sapiens chromosom	Homo sapiens chromosom
1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01
*** SEQUENCING IN PROG	*** SEQUENCING IN PROG	*** SEQUENCING IN PROG	*** SEQUENCING IN PROG	*** SEQUENCING IN PROG	*** SEQUENCING IN PROG	*** SEQUENCING IN PROG	*** SEQUENCING IN PROG	*** SEQUENCING IN PROG	*** SEQUENCING IN PROG
1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01	1.67e+01

ALIGNMENTS

RESULT	LOCUS	1	HUMHPBS	821 bp	mRNA	PRI	20-DEC-1993
DEFINITION	Human peripheral benzodiazepine receptor (hpbs) mRNA, complete cds.						
ACCESSION	M36035						
NID	g184333						
KEYWORDS	peripheral benzodiazepine receptor.						
SOURCE	Human cDNA to mRNA.						
ORGANISM	Homo sapiens						
REFERENCE	1 (Bases 1 to 821)						
AUTHORS	Riond, J., Mattei, M.G., Kaghad, M., Dumont, X., Guillemot, J.C., Le Fur, G., Caput, D. and Ferrara, P.						
TITLE	Molecular cloning and chromosomal localization of a human peripheral-type benzodiazepine receptor						
JOURNAL	Eur. J. Biochem. 195 (2), 305-311 (1991)						
MEDLINE	91146565						
REFERENCE	2 (bases 1 to 821)						
AUTHORS	Riond, J.						
TITLE	Direct Submission						
JOURNAL	Submitted (27-JUN-1990) J. Riond, Sanofi Elf Bio-Recherches, BP137, 31328 Labège Cedex, France						
FEATURES	Location/Qualifiers						
SOURCE	1..821						
	/organism="Homo sapiens"						
	/db_xref="taxon:9606"						
	/cell_line="hytciotyctic lymphoma monocytic-like cell line U937"						
	/clone="p-hpBS11"						
mRNA	<1..811						
	/note="peripheral benzodiazepine receptor mRNA"						
CDS	62..571						
	/codon_start=1						
	/note="peripheral benzodiazepine receptor"						
	/db_xref="PID:g306883"						
	/translation="MAPPPWPAMGFTLAPSLGCFVGSFRFVHGSLRWACGLQRPWSHP PHWLVGPVWGTLYSAMGYSLYWKELGGTEKAVPLVLTGQLALNWAAPDIFFGA RQMGWALVDLLVSGAAATTAAYQVSPLAARLLPYLAWLAFATLTTCVVRDNGH WHGGRRLPE"						

[illegible]

RESULT	2	HUMBENZA	639 bp	mRNA	PRI	20-MAY-1994
LOCUS		Human peripheral benzodiazepine receptor related mRNA sequence.				
DEFINITION		L21950				
ACCESSION		g483401				
NID		benzodiazepine receptor; peripheral benzodiazepine receptor.				
KEYWORDS		Homo sapiens cDNA to mRNA.				
SOURCE		Homo sapiens				
ORGANISM		Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
REFERENCE		1. (bases 1 to 639)				
AUTHORS		Lin, D., Chang, Y.J., Strauss, J.F. and Miller, W.L.				
TITLE		The human peripheral benzodiazepine receptor gene: cloning and characterization of alternative splicing in normal tissues and in a patient with congenital lipid adrenal hyperplasia				
JOURNAL		Genomics 18 (3), 643-650 (1993)				
MEDLINE		94140364				
FEATURES		Location/Qualifiers				
source		1. .639				
		/organism="Homo sapiens"				

CDS	polyA_site	BASE COUNT	100 a	201 c	200 g	138 t	ORIGIN
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161. .469							
/codon_start=1							
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/db_xref="PID:g488420"							
/translation="MAPHLLWCPTNGLGCGSPAGWGCGSHYRGLYPGPAGPPALPLPLAGLRDHTOLLRMAGOPWLAWGTAAARVSARPTRDCSTSRCHHACDVVAUTLS"							
639							
Query Match	83.1%;	Score 542;	DB 21;	Length 639;			
Best Local Similarity	99.5%;	Pred. No. 0.00e+00;					
Matches	545;	Conservative	0;	Mismatches	3;	Indels	0; Gaps
Db	61	GGTAGGGCTCTACTGTGCTGTGGAAGAGCTGGGAGGCTTCACAGAGAAGCTGTGGTTC	120				
Qy	105						
Db	121	CCCTGGGCTCTACACTGGGACAGCTGGCCCTGAACTGGGCATGGCCCCATCTCTCTTTG	180				
Qy	165	CCCTGGGCTCTACACTGGGACAGCTGGCCCTGAACTGGGCATGGCCCCATCTCTCTTTG	224				
Db	181	GTGCCCCAATAATGGGCTGGGCTTGGTGATCTCTGCTGGTCAGTGGGGGGGGGCGAG	240				
Qy	225	GTGCCCCAATAATGGGCTGGGCTTGGTGATCTCTGCTGGTCAGTGGGGGGGGGCGAG	284				
Db	241	CCACTACCGTGGCCTGTGTACAGAGTGAAGCCGCTGGCCGCGCTGCTACCCCTACC	300				
Qy	285	CCACTACCGTGGCCTGTGTACAGAGTGAAGCCGCTGGCCGCGCTGCTACCCCTACC	344				
Db	301	TGGCTTGCTGGCTTCCGGACACACTCACTACTTGGGTATGGGGGACAAACATGGCT	360				
Qy	345	TGGCTTGCTGGCTTCCAGCACCACTCAACTACTTGGGTATGGGGGACAAACATGGCT	404				
Db	361	GGCATGGGGGACGGCGCTGCCAGAGTCAGTGCCTGGCCGCCACACGGGACTGCAGCTGCAC	420				
Qy	405	GCGTGGGGGACGGCGCTGCCAGAGTCAGTGCCTGGCCGCCACACGGGACTGCAGCTGCAC	464				
Db	421	CAGCAGTGCCATCACGCTTGTGATGTGGTGGCGCTCAGCTTTTCATGACCACATGGGCT	480				
Qy	465	CAGCAGTGCCATCACGCTTGTGATGTGGTGGCGCTCAGCTTTTCATGACCACATGGGCT	524				
Db	481	GCTAGTCTGTAGGGCCCTTGGCCAGGGGTGAGCAGAGCTTCAGAGGTGGCCCACTGA	540				
Qy	525	GCTAGTCTGTAGGGCCCTTGGCCAGGGGTGAGCAGAGCTTCAGAGGTGGCCCACTGA	584				
Db	541	GGCCCAACCCGGGACAGTGTCTGTGCTTTCTGATCTTAGACATGTTCTTGGAAACA	600				
Qy	585	GGCCCAACCCGGGACAGTGTCTGTGCTTTCTGATCTTAGACATGTTCTTGGAAACA	644				
Db	601	TGGAATTT	608				
Qy	645	TGGAATTT	652				

RESULT	3	HSPBR4	684 bp	DNA	PRI	20-MAY-1994
LOCUS		Human peripheral benzodiazepine receptor gene, exon 4.				
DEFINITION						
ACCESSION		L21954				
KEYWORDS		9483405				
KEYWORDS		benzodiazepine receptor; peripheral benzodiazepine receptor.				
SEGMENT		4 of 4				
SOURCE		Homo sapiens DNA.				
ORGANISM		Homo sapiens				
REFERENCE		Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 684)				
REFERENCE		Liu, D., Chang, Y.J., Strauss, J.F. and Miller, W.L.				
AUTHORS		The human peripheral benzodiazepine receptor gene: cloning and				
TITLE						

characterization of alternative splicing in normal tissues and in a patient with congenital lipid adrenal hyperplasia
Genomics 18, 643-650 (1993)

JOURNAL MEDLINE 94140364

FEATURES Location/Qualifiers

source 1..684
/organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="placenta"
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join(L21952:195..376,L21953:224..362,164..352)
/codon_start=1
/product="peripheral benzodiazepine receptor"
/db_xref="PID:9488425"
/translation="MAPPPWPMAMFTGLAPSLGCFVSGFRVHGELRWYAGLQKPSWHP
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WHGERRLPE"
164..502

CDS join(L21952:195..376,L21953:224..362,164..352)

exon
BASE COUNT 113 a 200 c 225 g 146 t
ORIGIN

Query Match 61.8%; Score 403; DB 21; Length 684;
Best Local Similarity 99.3%; Pred. No. 3.85e-288;
Matches 406; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 163 GGCCTGTGGATCCCTGCTGAGTGGGCGCGCAGCAGCTACCTGGCTGGCTGTA 222
|||||
Qy 244 GGCCTGTGGATCCCTGCTGAGTGGGCGCGCAGCAGCTACCTGGCTGGCTGTA 303
|||||
Db 223 CCAGGTGAGCCCGCTGGCGCGCGCTGCTTACCCCTACCTGGCTGGCTGGCTTCCG 282
|||||
Qy 304 CCAGGTGAGCCCGCTGGCGCGCGCTGCTTACCCCTACCTGGCTGGCTGGCTTCC 363
|||||
Db 283 GACACACTCAACTACTGCTGATGGCGGAGACACATGGCTGGCATGGGGAGCGCGCT 342
|||||
Qy 364 GACACACTCAACTACTGCTGATGGCGGAGACACATGGCTGGCTGGGGAGCGCGCT 423
|||||
Db 343 GCACAGTGAAGTGGCGCGCGCAGCAGGACTGCAGCTGCACAGCAGGTGCATCAGCCT 402
|||||
Qy 424 GCCAGAGTGAAGTGGCGCGCGCAGCAGGACTGCAGCTGCACAGCAGGTGCATCAGCCT 483
|||||
Db 403 TGTGATGTGGTGGCGCTCACGCTTTTCATGACACTGGGCTGCTAGTGTGTCAGGGCCTT 462
|||||
Qy 484 TGTGATGTGGTGGCGCTCACGCTTTTCATGACACTGGGCTGCTAGTGTGTCAGGGCCTT 543
|||||
Db 463 GCGCCAGGGGTTCAGAGCTTCAGAGGTGGCCACCTGAGCCCCACCGCGGAGCAGT 522
|||||
Qy 544 GCGCCAGGGGTTCAGAGCTTCAGAGGTGGCCACCTGAGCCCCACCGCGGAGCAGT 603
|||||
Db 523 GTCCGTGCTTCTTCATGCTTAGAGCATGTTCTTGGAAACATGGAATTT 571
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Qy 604 GTCCGTGCTTCTTCATGCTTAGAGCATGTTCTTGGAAACATGGAATTT 652
|||||

RESULT 4
LOCUS HS1191B2 160559 bp DNA HTG 25-MAR-1998
DEFINITION Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone
1191B2; HTGS phase 1.

ACCESSION AL022237

NID 92995178

KEYWORDS HTG; HTGS_PHASE1.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 160559)

AUTHORS Sulston,J.

TITLE Direct Submission

JOURNAL Submitted (23-MAR-1998) Wellcome Trust Genome Campus, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

COMMENT

IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate segments. Unfinished sequence: bk1191B2 Contig_ID: 01719 acc= Length: 2099 bp Unfinished sequence: bk1191B2 Contig_ID: 01607 acc= Length: 5280 bp Unfinished sequence: bk1191B2 Contig_ID: 01221 acc= Length: 1033 bp Unfinished sequence: bk1191B2 Contig_ID: 01005 acc= Length: 1183 bp Unfinished sequence: bk1191B2 Contig_ID: 01520 acc= Length: 1158 bp Unfinished sequence: bk1191B2 Contig_ID: 01212 acc= Length: 1243 bp Unfinished sequence: bk1191B2 Contig_ID: 00949 acc= Length: 6912 bp Unfinished sequence: bk1191B2 Contig_ID: 00953 acc= Length: 3574 bp Unfinished sequence: bk1191B2 Contig_ID: 00946 acc= Length: 4065 bp Unfinished sequence: bk1191B2 Contig_ID: 00376 acc= Length: 2336 bp Unfinished sequence: bk1191B2 Contig_ID: 00587 acc= Length: 2115 bp Unfinished sequence: bk1191B2 Contig_ID: 00546 acc= Length: 3119 bp Unfinished sequence: bk1191B2 Contig_ID: 01145 acc= Length: 3772 bp Unfinished sequence: bk1191B2 Contig_ID: 01831 acc= Length: 5422 bp Unfinished sequence: bk1191B2 Contig_ID: 01683 acc= Length: 5648 bp Unfinished sequence: bk1191B2 Contig_ID: 01825 acc= Length: 9110 bp Unfinished sequence: bk1191B2 Contig_ID: 01829 acc= Length: 12009 bp Unfinished sequence: bk1191B2 Contig_ID: 00990 acc= Length: 14198 bp Unfinished sequence: bk1191B2 Contig_ID: 00103 acc= Length: 17541 bp Unfinished sequence: bk1191B2 Contig_ID: 01695 acc= Length: 20537 bp Unfinished sequence: bk1191B2 Contig_ID: 00329 acc= Length: 5642 bp Unfinished sequence: bk1191B2 Contig_ID: 00606 acc= Length: 8010 bp Unfinished sequence: bk1191B2 Contig_ID: 01248 acc= Length: 1799 bp Unfinished sequence: bk1191B2 Contig_ID: 00095 acc= Length: 4354 bp.

*** WARNING: Phase 1 High Throughput Genome Sequence ***

*** This sequence is unfinished. When sequencing is complete, * the sequence data presented in this record will be replaced *by a single finished sequence with the same accession number.

FEATURES source

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/db_xref="taxon:9606"
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/clone="1191B2"

BASE COUNT 33840 a 38651 c 38486 g 31167 t 18415 others
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Best Local Similarity 99.3%; Pred. No. 3.85e-288;
Matches 406; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 71240 AAATTCATGTTCCAGAACATGCTCTAAGCATGCACAAAGCAGGACACTGCTCCGG 71299
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Db 71300 GTGGGGCTCAGGTGGGGCCACCTCTGAGCTCTGCTGACCCCTGGGCCAAGGCCCTGAC 71359
Cp 592 GTGGGGCTCAGGTGGGGCCACCTCTGAGCTCTGCTGACCCCTGGGCCAAGGCCCTGAC 533
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Db 71360 AGACTAGCACGCCAGTGGTGCATGAAGCGCTGACGGCCACACATCAACAGCGTGATGGC 71419
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Cp 472 ACCTGCTGGTGACGTGAGTCCCTGTGGGCGGGGACTCCTGCTGGCAGCCGCCGTC 413
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Cp 412 CCCACGCCAGCGTGTGTCGCCCATACCGACTAGTTGAGTGTGTCGCGAAGGCCAG 353
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sequence: dJ526114 Contig_ID: 00896 Length: 751 bp.
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*** WARNING: Phase 1 High Throughput Genome Sequence ***
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* This sequence is unfinished. When sequencing is complete.
* the sequence data presented in this record will be replaced
* by a single finished sequence with the same accession number.
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    Matches 404; Conservative 0; Mismatches 5;
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Db 134181 TACCAGGTGAGCCGCTGGCCCGCGCTGTATACCCCTACCTGGCTGGCTGGCTTC 134240
QY 302 TACCAGGTGAGCCGCTGGCCCGCGCTGTCTACCCCTACCTGGCTGGCTGGCTTC 361
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QY 422 CTGCCAGAGTGAGTCCCGGCGCCACAGGAGCTGCAGCTGCACAGAGTGCCATCAG 481
Db 134361 CTTGNTGATGTGGTGGCGCTCACGCTTTTCATGACACTGGCGCTGTAGTCTGTGAGGGC 134420
QY 482 CTTG-TGATGTGGTGGCGCTCACGCTTTTCATGACACTGGCGCTGTAGTCTGTGAGGGC 540
Db 134421 CTTGGCCAGGGGTAGCAGAGCTTCAGAGGTGGCCCCACCTGAGCCCCCAGCCGCGGAGC 134480
QY 541 CTTGGCCAGGGGTAGCAGAGCTTCAGAGGTGGCCCCACCTGAGCCCCCAGCCGCGGAGC 600
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Db 134481 AGTGTCTGTGCTTTTCTGTCATGCTTAGAGCATGTTCTTGGACATGGAATTT 134532
QY 601 AGTGTCTGTGCTTTTCTGTCATGCTTAGAGCATGTTCTTGGACATGGAATTT 652

RESULT 7
LOCUS BOVPRIRBP 821 bp mRNA 05-AUG-1991
DEFINITION Calf peripheral-type benzodiazepine receptor isoquinoline binding protein (PBR/IBP) mRNA, complete cds.
ACCESSION M64520
NID 9163488
KEYWORDS benzodiazepine receptor isoquinoline binding protein.
SOURCE Calf adrenal gland, cDNA to mRNA.
ORGANISM Bos taurus
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Artiodactyla; Ruminantia; Pecora; Bovidea; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 821)
AUTHORS Parola,A.L., Stump,D.G., Pepper,D.J., Krueger,K.E., Regan,J.W. and Laird,H.E.II.
TITLE Cloning and expression of a pharmacologically unique bovine peripheral-type benzodiazepine receptor isoquinoline binding protein
JOURNAL J. Biol. Chem. 266, 14082-14087 (1991)
MEDLINE 91310699
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Db 204 CTGGATTCCTGCCCTCCCATCTGGGGCACACACTCTACTCGGCCATGGGGTATGTTCTACAT 263
QY 61 CTGGGTCTGGGGCCTGTCTGGGGCACGCTCTACTCAGCCATGGGGTACGGCTCTACCT 120
Db 264 GATCTGGAAGAGCTGGGGGCTTCTCGAAGAGGGCGGTGTTCCCTGGGCTCTACGC 323
QY 121 GGCTGGAAGAGCTGGGAGGCTTCACAGAGAAGGCTGTGTTCCCTGGGCTCTACAC 180
Db 324 TGGCAGCTGGCTCTGAACCTGGGCATGGCTCCCTCTCTTCTGGGCACCTCGACAAATGGG 383
QY 181 TGGCAGCTGGCCTTGAACTGGGCATGGCCCGCCCATCTCTTTGGTCCCGCACAAATGGG 240
Db 384 CTGGGCCCTTGGTGGATCTCTCTGTGACTGGCGGCATGGACAGACCCAGCCGATGGCGCTG 443
QY 241 CTGGGCCCTTGGTGGATCTCTCTGTGCTGAGTGGCGGCGGCGGAGCCACTACCGTGGCGTG 300
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Db 444 GCACAGGTGAGCCCGCGGCTGCTGCTGTGTACCTGACCTGGCTGGCTGGCTT 503
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Db 504 TCCCGGCGTCTCACTACCTACCGATGTGCGAGACACACAGTCGGAGGATGCGCGCG 563
Qy 361 CACGACCACTCACTACTCGTATCGTGGGACAAACATGGCTGGCTGGGGACGCG 420

Db 564 GCTCTCGGAATGAGCAGCCCTCGCGCTCCGAGGAGCTGCAGCGC 607
Qy 421 CTTGCCAGATGAGTGC-CCG-GCCACACAGGAGCTGCAGCTGC 462

RESULT 8
LOCUS MUSMPBR 626 bp mRNA ROD 27-JUL-1994
DEFINITION Mouse peripheral-type benzodiazepine receptor mRNA, complete cds.
ACCESSION L17306
NID 9309441
KEYWORDS benzodiazepine receptor.
SOURCE Mus musculus mouse testis tumor cdNA to mRNA.
ORGANISM Mus musculus
Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.
REFERENCE 1 (bases 1 to 626)
AUTHORS Garnier, M., Dimchev, A.B., Boujrad, N., Price, J.M., Musto, N.A. and Papadopoulos, V.
TITLE In vitro reconstruction of a functional peripheral-type benzodiazepine receptor from mouse Leydig tumor cells
JOURNAL Mol. Pharmacol. 45 (2), 201-211 (1994)
MEDLINE 94158796
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Best Local Similarity 80.4%; Pred. No. 8,06e-192;
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Db 112 GCGAGGCGCTCCGGTGTATGCTAGCTTGCAGAAACCTCTTGGCATCCGCTCGCTGG 171
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Db 172 ACATGGCTCCCATCTGGGGCACACTGTATTACGACCATGGGTATGGCTCTACATAGTC 231
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Db 232 TGGAAAGAGCTGGGAGGTTTACAGAGACCGCTATGGTTCCCTTGGGTCTCTACACTGGT 291
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Db 352 GCCTTGGCCGATCTTCTGCTTGTGTCAGTGGGGTGGCGACTGCCAACACCTGGCTGGCAC 411
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Db 412 CGAGTGAGCCCGCGGCTGCCCTTGTCTGTACCTTACCTGGCTGGCTGGCTTGGCC 471
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Qy 365 ACCACACTCAACTACTGCGTATGCGGAGCAACATGGTGGTGGGAGCGCGCTG 424

Db 532 CCAGAGTGAAGGACCCAGCCATCAGGAATGCAGCCCTGCCAGC 575
Qy 425 CCAGAGTGAAGTGGCGCGGCCACCAGGAGCTGCAGCTGCACCAGC 468

RESULT 9
LOCUS RATPKBSX 781 bp mRNA ROD 12-JUN-1992
DEFINITION Rat peripheral-type benzodiazepine receptor (PKBS) mRNA, complete cds.
ACCESSION J05122
NID 9206161
KEYWORDS peripheral-type benzodiazepine receptor.
SOURCE Rat adult adrenal cortex, cdNA to mRNA.
ORGANISM Rattus norvegicus
Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Rattus.
REFERENCE 1 (bases 1 to 781)
AUTHORS Sprengel, R., Werner, P., Seeburg, P.H., Mukhin, A.G., Santi, M.R., Grayson, D.R., Guidotti, A. and Krueger, K.E.
TITLE Molecular cloning and expression of cDNA encoding a peripheral-type benzodiazepine receptor
JOURNAL J. Biol. Chem. 264, 20415-20421 (1989)
MEDLINE 90062173
COMMENT Draft entry and computer readable copy of sequence [1] kindly provided by Krueger, K.E., 20-SEP-1989.
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Db 116 GGTGAGGGCTCCGCTGGTATGCTAGCTTGCAGAAACCTCTCTGGCATCCGCTCGCTG 175
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Qy 65 GTGCTGGGCCCTGTCTGGGGCAGCTTACTACGACCATGGGTACGGCTCTACCTGGTC 124

Db 236 TGGAAAGAGCTGGGAGGTTTACAGAGAGGCTTACAGAGAGGCTGTGGTTCCCTTGGGCTCTACACTGGT 295
Qy 125 TGGAAAGAGCTGGGAGGCTTACAGAGAGGCTGTGGTTCCCTTGGGCTCTACACTGGG 184

Db 296 CAGCTGGCTCTGAACCTGGGATGGCCCCCATCTCTTTGGTGGCCGCGCATGGGCTGG 355
Qy 185 CAGCTGGCCCTGAACCTGGGATGGCCCCCATCTCTTTGGTGGCCGCGCAAAATGGGCTGG 244

Db 356 GCCTTGGTGGACCTCATGCTGTGTCAGTGGGTGGCAACCGCCACTACCTGGCTGGCAC 415
Qy 245 GCCTTGGTGGATCTCCTGCTGTCAGTGGGGCGGCGGCGGCGGCGGCGGCGGCTGCTAC 304

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QY 245 GCCTTGGTGGATCTCCTGCTGGTCAGTGGGGGGGGGAGCCACTACCGTGGCTGGTAC 304

Db 416 CGAGTAGAGCCACCGGTGCCCCGTGCTGATCTTACCTGGGCTGGCTGGCTTTGCC 475

QY 305 CAGGTAGCCGGCTGGCCGGCCGCTGCTACCCCTACCTGGCTGGCTGGCTTACG 364

Db 476 ACCATGCTCACTACTATGATGGGTGATACACTCTGGTGGGAGGGGGTCCCGGCTC 535

QY 365 ACCACACTCACTACTGCTATGGCGGACCAACCATGGCTGGCGTGGGGGAGCGCGCTG 424

Db 536 ACAGAGTGAG 545

QY 425 CCAGAGTGAG 434

RESULT 10 MUSPTR 856 bp mRNA ROD 27-MAR-1996

LOCUS Mouse mRNA for peripheral-type benzodiazepine receptor, complete

DEFINITION cds

ACCESSION D21207

NID 9484053

KEYWORDS peripheral-type benzodiazepine receptor.

SOURCE Mus musculus Cell-line erythro leukemia (library: lambda gt11) cDNA to mRNA.

ORGANISM Mus musculus

REFERENCE Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Taketani,S., Kohno,H., Okuda,M., Furukawa,T. and Tokunaga,R.

TITLE Induction of peripheral-type benzodiazepine receptors during differentiation of mouse erythro leukemia cells. A possible involvement of these receptors in heme biosynthesis

JOURNAL J. Biol. Chem. 269, 2527-7531 (1994)

REFERENCE 2 (bases 1 to 856)

AUTHORS Taketani,S.

TITLE Direct Submission

JOURNAL Submitted (15-OCT-1993) to the DDBJ/EMBL/GenBank databases. Shigeru Taketani, Kansai Medical University, Dept. of Hygiene; 10-15 Fumizono-cho, Moriguchi, Osaka 570, Japan

COMMENT Submitted (15-Oct-1993) to DDBJ by: Shigeru Taketani

Department of Hygiene

Kansai Medical University

1-Fumizonocho, Moriguchi

Osaka 570

Japan

Phone: 06-992-1001 x2504

Fax: 06-992-3522.

FEATURES

Location/Qualifiers

1. 856

/organism="Mus musculus"

/strain="BALB/c"

/sub_species="domesticus"

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Best Local Similarity 79.5%; Pred. No. 1.71e-185;

Matches 369; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

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QY 5 GGGAGAGGCTCCGGTGGTATGCTAGCTTCAGAAAACCCCTCGTGGCACCCGCCCCACTGG 64

Db 207 ACAGTGGCTCCCATCTGGGCAACACTGTATACGCCATGGGGTATGGCTCTACATAGTC 266

QY 65 GTGCTGGGCGCTGTCTGGGCGACGCTCTACTACGCCATGGGGTACGGCTCTACCTGGTC 124

Db 267 TGAAGAGAGCTGGAGGTTTTCACAGAGGAGCGCTATGGTTCCCTTGGGTCTCTACACTGGT 326

QY 125 TGAAGAGAGCTGGAGGCTTCACAGAGAGGCTGTGGTTCCCTTGGGCTCTACACTGGG 184

Db 327 CAGCTGGCTCTGAACACTGGGCGTGGCCCCCATCTTCTTTGGTCCCGGCGAGATGGGTGG 386

QY 185 CAGCTGGCGCTGAACACTGGGCGATGGCCCCCATCTTCTTTGGTGGCGGCAAAATGGGCTG 244

Db 387 GCCTTGGCGCATCTTCTGCTGTGTCAGTGGGGTGGCGACTGCCACACCCCTGGCTGGCAC 446

QY 245 GCCTTGGTGGATCTCTGCTGGTGGTGGGGCGGCGACGACCTACCGTGGCGTGGTAC 304

Db 447 CGAGTAGAGCGCGCGCTGCGCGCTGTGCTGTACCTTACCTTACCTGGCTGGCTTTGGCC 506

QY 305 CAGTGAGCGCGCTGGCGCGCGCTGCTCTACCCCTACCTGGCTGGCTGGCTTCAGC 364

Db 507 ACCGTGCTCAACTACTATGATGGCGTGTATGCTGTAACTCTTGGCGCGAGGGGCTCCCGGCTC 566

QY 365 ACCACACTCAACTACTGCGTATGGCGGACCAACCATGGCTGGTGGGACGCGGCTG 424

Db 567 GCAGAGTAGAGGACCCAGCCATCAGGAATGCAGCCCTGCCAGC 610

QY 425 CCAGAGTAGTGCCCGCGCCACCAGGAGCTGCAGCTGCACCAGC 468

RESULT 11 HSPB3 645 bp DNA PRI 20-MAY-1994

LOCUS Human peripheral benzodiazepine receptor gene, exon 3.

DEFINITION L21953

ACCESSION 9483404

NID

KEYWORDS benzodiazepine receptor; peripheral benzodiazepine receptor.

SEGMENT 3 of 4

SOURCE Homo sapiens DNA.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 645)

AUTHORS Lin,D., Chang,Y.J., Strauss,J.F. and Miller,W.L.

TITLE The human peripheral benzodiazepine receptor gene: cloning and characterization of alternative splicing in normal tissues and in a patient with congenital lipoid adrenal hyperplasia

JOURNAL Genomics 18, 643-650 (1993)

MEDLINE 94140364

FEATURES

Location/Qualifiers

1. 645

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/db_xref="taxon:9606"

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/product="peripheral benzodiazepine receptor"

BASE COUNT 138 a 177 c 192 g 138 t

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Best Local Similarity 98.6%; Pred. No. 6.34e-72;

Matches 140; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

Db 223 GGTACGGCTCTCTACCTGGTCTGGAAGAGTGGGAGGCTTCACAGAGAAGCTGTGGTT 282

QY 105 GGTACGGCTCTCTACCTGGTCTGGAAGAGTGGGAGGCTTCACAGAGAAGCTGT-GGTT 163

Db 283 CCCTGGCGCTCTACTTGGGAGCTGGCGCTGAACTGGGCGATGGCCCCCATCTTCTT- 341

QY 164 CCCTGGGCTCTACACTGGGAGCTGGCCCTGAACCTGGGCGATGGCCCCCATCTTCTTT 223

Db 342 GGTGCCCCGACAAATGGGCTGGG 363
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QY 224 GGTGCCCCGACAAATGGGCTGGG 245
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RESULT 12
LOCUS RATPTB2R02 3434 bp DNA ROD 25-JAN-1993
DEFINITION Rat peripheral-type benzodiazepine receptor gene exons 2-4,
complete cds.
ACCESSION M84221
NID 9206478
KEYWORDS peripheral-type benzodiazepine receptor.
SEGMENT 2 of 2
SOURCE Rattus norvegicus (strain Wistar) Adult DNA.
ORGANISM Rattus norvegicus
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Rattus.
REFERENCE 1 (bases 1 to 3434)
AUTHORS Sprengel,R., Werner,P., Seeburg,P.H., Mukhin,A.G., Santi,R.M.,
Grayson,D.R., Guldotti,A. and Krueger,K.E.
TITLE Molecular Cloning and Expression of cDNA Encoding a Peripheral-type
Benzodiazepine Receptor
JOURNAL J. Biol. Chem. 264, 20415-20421 (1989)
MEDLINE 90062173
REFERENCE 2 (bases 1 to 3434)
AUTHORS Casalotti,S.O., Pelaia,G., Yakovlev,A.G., Csikos,T., Grayson,D.R.
and Krueger,K.E.
TITLE Structure of the rat gene encoding the mitochondrial benzodiazepine
receptor
JOURNAL Gene 121, 377-382 (1992)
MEDLINE 93077057
COMMENT Sequence M84221 starts with a Bam HI site, leaving a gap of about
7kb between sequences.
FEATURES
source Location/Qualifiers
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exon 2066..2924
intron 2925..3350
exon 713 a 872 c 991 g 858 t
BASE COUNT 713 a 872 c 991 g 858 t
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Query Match 17.6%; Score 115; DB 23; Length 3434;
Best Local Similarity 90.8%; Pred. No. 3.97e-62;
Matches 128; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
Db 1926 GGTATGGCTCTACATATCTGGAAGAGCTGGGAGTTTCACAGAGAGCTATGCTTC 1985
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QY 105 GGTACGGCTCTACCTGGTGTGGAAGAGCTGGGAGGCTTTCACAGAGAGGCTGTGTTTC 164

Db 1986 CCTTGGGCTCTCTACACTGGTCAGCTGCTGAACCTGGGCGATGGCCCCCATCTTCTTTG 2045
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QY 165 CCTGGGCCCTCTACACTGGGCGAGCTGGCCCTGAACCTGGGCGATGGCCCCCATCTTCTTTG 224
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Db 2046 GTGCCCCGACAGATGGGCTGGG 2066
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QY 225 GTGCCCCGACAAATGGGCTGGG 245
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RESULT 13
LOCUS HSPBR2 487 bp DNA PRI 20-MAY-1994
DEFINITION Human peripheral benzodiazepine receptor gene, exon 2.
ACCESSION L21952
NID 9483403
KEYWORDS benzodiazepine receptor; peripheral benzodiazepine receptor.
SEGMENT 2 of 4
SOURCE Homo sapiens DNA.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 487)
AUTHORS Lin,D., Chang,Y.J., Strauss,J.F. and Miller,W.L.
TITLE The human peripheral benzodiazepine receptor gene: cloning and
characterization of alternative splicing in normal tissues and in a
patient with congenital lipid adrenal hyperplasia
JOURNAL Genomics 18, 643-650 (1993)
MEDLINE 94140364
FEATURES
source Location/Qualifiers
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Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 272 CCACGGCAGGGTCTCCGCTGGTACCGCGCTGCGAGAGCCCTGCTGCGACCCGCCCA 331
QY 1 CCACGGCAGAGTCTCCGCTGGTACCGCGCTGCGAGAGCCCTGCTGCGACCCGCCCA 60
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Db 332 CTGGGTGCTGGGCCCTGTCTGGGGCAGCGCTACTACTCAGCCATGGGTA 379
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QY 61 CTGGGTGCTGGGCCCTGTCTGGGGCAGCGCTACTACTCAGCCATGGGTA 108
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RESULT 14
LOCUS I66494 7218 bp DNA PAT 23-DEC-1997
DEFINITION Sequence 14 from patent US 5670367.
ACCESSION I66494
NID 92724471
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 7218)
AUTHORS Dörner,F., Scheiflinger,F. and Falkner,F.Gunter.
TITLE Recombinant fowlpox virus
JOURNAL Patent: US 5670367-A 14 23-SEP-1997;
FEATURES
source Location/Qualifiers
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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Jul 21 15:37:35 1998; MasPar time 830.75 Seconds
1309.640 Million cell updates/sec

Tabular output not generated.

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Description: (1-652) from US09047652A.seq
Perfect Score: 652
N.A. Sequence: 1 CCACGGCGAGGCTCTCCGCT.....GTTCTTGGACATGGAATT 652
Comp: GGTGCGCGTCCGAGGCGCA.....CAAGAACCTTGACCTTAA

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 457396 seqs, 834342348 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: emb154
1:em_ba 2:em_htg 3:em_hum1 4:em_hum2 5:em_in 6:em_om
7:em_or 8:em_ov 9:em_pat 10:em_pl 11:em_ro 12:em_v1
genbank106

Database: 13:gb_ba 14:gb_htg 15:gb_in 16:gb_om 17:gb_ov 18:gb_pat
19:gb_ph 20:gb_pl 21:gb_pr1 22:gb_pr2 23:gb_ro 24:gb_st
25:gb_sy 26:gb_un 27:gb_v1

Statistics: Mean 10.376; Variance 5.505; scale 1.885

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match	Pred. No.
1	645	98.9	821
2	542	83.1	839
3	403	61.8	639
4	403	61.8	160559
5	402	61.7	4258
6	384	58.9	152843
7	290	44.5	821
8	284	43.6	626
9	278	42.6	781
10	276	42.3	856
11	128	19.6	645
12	115	17.6	3434
13	108	16.6	487
14	39	6.0	7218
15	37	5.7	1084

LOCUS	1	HUMHPBS	821 bp	MRNA	PRI	20-DEC-1993
DEFINITION						
ACCESSION						
NID						
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
FEATURES						
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ALIGNMENTS

RESULT 1

LOCUS HUMHPBS 821 bp MRNA PRI 20-DEC-1993

DEFINITION Human peripheral benzodiazepine receptor (hpbs) mRNA, complete cds.

ACCESSION M36035

NID g184333

KEYWORDS peripheral benzodiazepine receptor.

SOURCE Human cDNA to mRNA.

ORGANISM Homo sapiens

REFERENCE Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 821)

AUTHORS Riond,J., Mattei,M.G., Kaghad,M., Dumont,X., Guillemot,J.C., Le Fur,G., Caput,D. and Ferrara,P.

TITLE Molecular cloning and chromosomal localization of a human peripheral-type benzodiazepine receptor

JOURNAL Eur. J. Biochem. 195 (2), 305-311 (1991)

MEDLINE 91146565

REFERENCE 2 (bases 1 to 821)

AUTHORS Riond,J.

TITLE Direct Submission

JOURNAL Submitted (27-JUN-1990) J. Riond, Sanofi Elf Bio-Recherches, BP137, 31328 Labège Cedex, France

FEATURES

1. 821

Location/Qualifiers

source

1. 821

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Best Local Similarity 99.1%; Pred. No. 0.00e+00;									
Matches 648; Conservative 0; Mismatches 4; Indels 0; Gaps 0;									
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Qy 61 CTGGGTCTGGCCCTGTCTGGGGCAGCTCTACTCAGCCATGGGCTCCTACTCT 120									
Db 259 GGTCTGAAAGAGCTGGAGGCTTACAGAGAGGCTGTGGTCCCTCGGGCTCTACAC 318									
Qy 121 GGTCTGAAAGAGCTGGAGGCTTACAGAGAGGCTGTGGTCCCTCGGGCTCTACAC 180									
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Db 499 CGCACCACACTCACTACTGCGTATGGCGGACACACCTGCTGCATGGGGGACGGG 558									
Qy 361 CACGACCACACTCACTACTGCGTATGGCGGACACACCTGCTGCATGGGGGACGGG 420									
Db 559 GCTGCCAGGTGAGTGGCCGCCGCCACAGGAGCTGCAGCTGCACACAGGTCGCCATCAC 618									
Qy 421 GCTGCCAGGTGAGTGGCCGCCGCCACAGGAGCTGCAGCTGCACACAGGTCGCCATCAC 480									
Db 619 GCTGTGATGTGGCCGCTCAGCTTTCATGACCACTGGCCCTGCTACTGTCTAGGGC 678									
Qy 481 GCTGTGATGTGGCCGCTCAGCTTTCATGACCACTGGCCCTGCTACTGTCTAGGGC 540									
Db 679 CTTGGCCAGGGTTCAGAGCTTTCAGAGTGGCCCACTGAGCCGCCACCCGGGAGC 738									
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Db 739 AGTGTCTGTCTTCTGCTATGTAGAGCATGTTCTTGGACATGGAATTT 790									
Qy 601 AGTGTCTGTCTTCTGCTATGTAGAGCATGTTCTTGGACATGGAATTT 652									
RESULT 2 HUMBENZA 639 bp mRNA PRI 20-MAY-1994									
LOCUS Human peripheral benzodiazepine receptor related mRNA sequence.									
DEFINITION L21950									
ACCESSION 9483401									
NID benzodiazepine receptor; peripheral benzodiazepine receptor.									
KEYWORDS Homo sapiens cDNA to mRNA.									
SOURCE Homo sapiens									
ORGANISM Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Euthera; Primates; Catarrhini; Hominiidae; Homo.									
REFERENCE 1 (bases 1 to 639)									
AUTHORS Lin,D., Chang,Y.J., Strauss,J.F. and Miller,W.L.									
TITLE The human peripheral benzodiazepine receptor gene: cloning and characterization of alternative splicing in normal tissues and in a patient with congenital lipid adrenal hyperplasia									
JOURNAL Genomics 18 (3), 643-650 (1993)									
MEDLINE 94140364 Location/Qualifiers									
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Cp 352 CCAGCCAGGTAGGGGTAGACAGCGGGCGCCAGCGGGCTACCTGGTACCAGGCCAC 293
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Db 71600 GGTAGTGGCTCCCGCCGCCACTGACACAGCAGGAGATCCACCAAGGCC 71648
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Cp 292 GGTAGTGGCTCCCGCCGCCACTGACACAGCAGGAGATCCACCAAGGCC 244
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RESULT 5
LOCUS HSU12421 4258 bp DNA PRI 14-DEC-1995
DEFINITION Human mitochondrial benzodiazepine receptor (MBR) gene, complete cds.
ACCESSION U12421
NID 9529945
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Euthera; Primates; Catarrhini; Homidae; Homo. 1 (bases 2080 to 3683)
REFERENCE
AUTHORS Yakovlev.A.G., Ruffo.M., Jurka.J. and Krueger.K.E.
TITLE Comparison of repetitive elements in the third intron of human and rodent mitochondrial benzodiazepine receptor-encoding genes
JOURNAL Gene 155 (2), 201-205 (1995)
MEDLINE 95237610
REFERENCE 2 (bases 1 to 4258)
AUTHORS Krueger,K.E.
TITLES Direct Submission
JOURNAL Submitted (19-JUL-1994) Karl E. Krueger, Dept. of Cell Biology, Georgetown University School of Medicine, Washington, DC 20007, USA
FEATURES
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/number=3
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ORIGIN

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Best Local Similarity 99.8%; Pred. No. 6,58e-287;
Matches 408; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Db 3683 GGCTTTGGTGGATCTCTGCTGCTGAGTGGGGCGGGGAGACCATGCTGGCGGGGACGGCGCT 3742
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QY 244 GGCTTTGGTGGATCTCTGCTGCTGAGTGGGGCGGGGAGACCATGCTGGCGGGGACGGCGCT 303
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QY 304 CCAGGTAGAGCCCGCTGGCGCCCGCTGCTTACCCCTACCTGGCTGGCTGGCTTCAC 363
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Db 3803 GACCACTCAACTACTGCTGATGGCGGGACACCATGCTGGCGGGGACGGCGCT 3862
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QY 364 GACCACTCAACTACTGCTGATGGCGGGACACCATGCTGGCGGGGACGGCGCT 423
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Db 3863 GCCAGAGTGTAGTCCCGGGCCACAGGAGCTGCAGCTGCACAGAGGTGCCATCAGCT 3922
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QY 424 GCCAGAGTGTAGTCCCGGGCCACAGGAGCTGCAGCTGCACAGAGGTGCCATCAGCT 483
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Db 3983 GGCCAGGGGTGACAGAGCTTCAGAGGTGGCCCCAC-TGAGCCCCACCCGGGAGCAGT 4041
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QY 544 GGCCAGGGGTGACAGAGCTTCAGAGGTGGCCCCACCTGAGCCCCACCCGGGAGCAGT 603
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QY 604 GTCTGTGCTTTCTGATGCTTAGAGCATGTTCTTGGAAATTT 652
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RESULT 6
LOCUS HS26114 152843 bp DNA HTG 13-JAN-1997
DEFINITION Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 526114; HTGS phase 1.
ACCESSION 282214
NID g1666406
KEYWORDS HTG; HTGS_PHASE1.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Euthera; Primates; Catarrhini; Homidae; Homo. 1 (bases 1 to 152843)
REFERENCE
AUTHORS Buck,D.
TITLE Direct Submission
JOURNAL Submitted (06-NOV-1996) Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquires: humquerry@sanger.ac.uk
COMMENT IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate segments. Unfinished sequence: dJ526114 Contig_ID: 00003 Length: 15560 bp Unfinished sequence: dJ526114 Contig_ID: 00229 Length: 791 bp Unfinished sequence: dJ526114 Contig_ID: 00240 Length: 810 bp Unfinished sequence: dJ526114 Contig_ID: 00248 Length: 750 bp Unfinished sequence: dJ526114 Contig_ID: 00250 Length: 763 bp Unfinished sequence: dJ526114 Contig_ID: 00263 Length: 794 bp Unfinished

QY	245	GCCTGTGGTATCTCTGCTGGTTCAGTGGGGCGGCGAGCCATACCGTGGCCTGGTAC	304
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QY	305	CAGTGAAGCCGCTGGCGCGGCTGCTCTACCCCTACCTTGGCTGGCTGGCCTTCAGG	364
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QY	365	ACCACTCAACTACTGCTATGGCGGACAAACATGCTGGCTGGGGAGCGGGCTG	424
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QY	425	CCAGAGTGAG	434
RESULT	10		
LOCUS	MUSPTBR	856 bp	RNA
DEFINITION	Mouse mRNA for peripheral-type benzodiazepine receptor, complete cds.		27-MAR-1996
ACCESSION	D21207		
NID	g484053		
KEYWORDS	peripheral-type benzodiazepine receptor.		
SOURCE	Mus musculus cell-line erythro leukemia (library: lambda gt11) cDNA to mRNA.		
ORGANISM	Mus musculus		
	Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 856)		
AUTHORS	Taketani,S., Kohno,H., Okuda,M., Furukawa,T. and Tokunaga,R.		
TITLE	Induction of peripheral-type benzodiazepine receptors during differentiation of mouse erythro leukemia cells. A possible involvement of these receptors in heme biosynthesis		
JOURNAL	J. Biol. Chem. 269, 2527-7531 (1994)		
REFERENCE	2 (bases 1 to 856)		
AUTHORS	Taketani,S.		
TITLE	Direct Submission		
JOURNAL	Submitted (15-Oct-1993) to the DDBJ/EMBL/GenBank databases. Shigeru Taketani, Kansai Medical University, Dept. of Hygiene, 10-15 Fumizono-cho, Moriguchi, Osaka 570, Japan		
	(Tel:06-992-1001(ex.2504), Fax:06-992-3522)		
COMMENT	Submitted (15-Oct-1993) to DDBJ by: Shigeru Taketani		
	Department of Hygiene		
	Kansai Medical University		
	1-Fumizonocho, Moriguchi		
	Osaka 570		
	Japan		
FEATURES	source		
	Phone: 06-992-1001 x2504		
	Fax: 06-992-3522.		
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BASE COUNT	150 a	253 g	199 t
ORIGIN	254 c		
Query Match	42.3%	Score 276;	DB 23; Length 856;
Best Local Similarity	79.7%	Pred. No. 8,60e-187;	
Matches	0;	Mismatches 94;	Indels 0; Gaps 0;

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Qy	5	GGCAGGGGTCTCCGCTGGTACGCCGGGCTGCAGAACCCCTCGTGGCACCGCGCCCACTGG	64
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Qy	65	GTGCTGGGCCCTGTCTGGGCACGCTCTACTCAGCCATGGGTACGGCTCTTACCTGGTC	124
Db	267	TGGAAGAGCTGGGAGGTTTCACAGAGAGCGCTATGGTTCCTCTGGTCTCTACACTGGT	326
Qy	125	TGGAAGAGCTGGGAGGCTTCACAGAGAAGCTGTGGTTCCTCGGCTCTACACTGG	184
Db	327	CAGCTGGCTCTGAACCTGGGCGTGGCCCCCATCTTTTGGTGCCCGGAGATGGGCTGG	386
Qy	185	CAGCTGGCCCTGAACCTGGGCATGGCCCCCATCTCTTTGGTGCCCGACAAATGGGCTGG	244
Db	387	GCCTTGGCCGATCTTCGCTTGTCACTGGGGTGGCGACTGCCACAACCCCTGGCTTGGCAC	446
Qy	245	GCCTTGTGTGATCTCTCTGGTCACTGGTGGGGCGGCGGACCCACTACCGTGGCTGGTAC	304
Db	447	CGAGTGAGCCCGCGCTGGCCGCTTGTCTACCCCTTACCTGGCCCTGGTGGCTTTTGCC	506
Qy	305	CAGGTGAGCCCGCTGGCGCGCTCTCTACCCCTACCTGGCTGGTGGCTTCACG	364
Db	507	ACCGTGTCAACTACTATGTATGGCGTGATACTCTGGCGGGGAGGGGGCTCCCGGCTC	566
Qy	365	ACCACATCAACTACTCCGTATGGCGGAGAACCATGGCTGGGCTGGGGACGGCGGCTG	424
Db	567	GCAGAGTGAAGGACCCAGCGCATCAGGAATGCAGCCCTGCCACG	610
Qy	425	CCAGAGTGAGTGCCCGGCCCCACAGGGACTGCAGCTGCACCAACG	468
RESULT	11	HSPBR3	
LOCUS		Human peripheral benzodiazepine receptor gene, exon 3.	
DEFINITION		645 bp DNA	PRI 20-MAY-1994
ACCESSION		L21953	
NID		g483404	
KEYWORDS		benzodiazepine receptor; peripheral benzodiazepine receptor.	
SEGMENT		3 of 4	
SOURCE		Homo sapiens	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;	
AUTHORS		Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
TITLE		1. (bases 1 to 645)	
		Lin, D., Chang, X.J., Strauss, J.F. and Miller, W.L.	
		The human peripheral benzodiazepine receptor gene: cloning and	
		characterization of alternative splicing in normal tissues and	
		patient with congenital lipid adrenal hyperplasia	
JOURNAL		Genomics 18, 643-650 (1993)	
MEDLINE		94140364	
FEATURES		Location/Qualifiers	
source		1. 645	
		/organism="Homo sapiens"	
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		/tissue_type="placenta"	
		/tissue_lib="placenta"	
		224..362	
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BASE COUNT		138 a 177 c 192 g 138 t	
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Query Match 19.6%; Score 128; DB 21; Length 645;			
Best Local Similarity 98.6%; Pred. No. 8.17e-72;			
Matches 140; Conservative 0; Mismatches 0; Indels 2; Gaps			
Db	223	GGTACGGCTCTACTCGTCTGGAAGAGCTGGAGGCTTCACAGAGAAGCGCTGTGGTT	282
Qy	105	GGTACGGCTCTACTCGTCTGGAAGAGCTGGAGGCTTCACAGAGAAGCGTGTGGTT	163
Db	283	CCCTGGGCGCTTCTACTGGGCGAGCTGGCCCTGNACTGGGCTACCGCCCATCTTCTT	341

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QY 164 CCCCTGGGCTCTACACTGGCAGCTGGCCCTGAACCTGGGCGATGGCCCCCATCTTCTTT 223
Db 342 GGTGCCGACAAATGGCTGGG 363
QY 224 GGTGCCGACAAATGGGCTGGG 245

RESULT 12
LOCUS RATPB2R02 3434 bp DNA ROD 25-JAN-1993
DEFINITION Rat peripheral-type benzodiazepine receptor gene exons 2-4,
complete cds.
ACCESSION M84221
NID g206478
KEYWORDS peripheral-type benzodiazepine receptor.
SEGMENT 2 of 2
SOURCE Rattus norvegicus (strain Wistar) Adult DNA.
ORGANISM Rattus norvegicus
Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Euthera; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Rattus.
REFERENCE 1 (bases 1 to 3434)
AUTHORS Sprengel, R., Warner, P., Seeburg, P.H., Mukhin, A.G., Santi, R.M.,
Grayson, D.R., Guidotti, A. and Krueger, K.E.
TITLE Molecular Cloning and Expression of cDNA Encoding a Peripheral-type
Benzodiazepine Receptor
J. Biol. Chem. 264, 20415-20421 (1989)
MEDLINE 90062173
REFERENCE 2 (bases 1 to 3434)
AUTHORS Casaliotti, S.O., Pelala, G., Yakovlev, A.G., Csikos, T., Grayson, D.R.
and Krueger, K.E.
TITLE Structure of the rat gene encoding the mitochondrial benzodiazepine
receptor
Gene 121, 377-382 (1992)
JOURNAL 93077057
MEDLINE
COMMENT Sequence M84221 starts with a Bam HI site, leaving a gap of about
7Xb between sequences.
FEATURES
source
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/organism="Rattus norvegicus"
/strain="Wistar"
/db_xref="taxon:10116"
/dev_stage="adult"
/number=1
intron order(M95864:1273..1462,1..1094)
prim_transcript 1..3350
exon 1095..1305
/number=2
/number=1
join(1124..1305,1927..2065,2925..3113)
/number=2
/number=1
/codon_start=1
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/db_xref="PID:g206480"
/translation="MSQSWPAPVGLTLVPSLGMFGAYFVRGGLRWYASLQKPSWHP
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RRGWSRLTE"
intron 1306..1926
exon /number=2
1927..2065
/number=3
intron 2066..2924
/number=3
2925..3350
exon /number=4
BASE COUNT 713 a 872 c 991 g 858 t
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Best Local Similarity 90.8%; Pred. No. 4.95e-62;
Matches 128; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Db 1926 GGTATGGCTCTACATAATCTGGAAGAGCTGGGAGGTTTTCACAGAGGAGGCTATGGTTC 1985
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QY 105 GGTACGGCTCTACCTGCTGTGGAAGAGCTGGGAGGCTTCACAGAGAAGGCTGTGGTTC 164
Db 1986 CCTTGGGCTCTACACTGGTCTGAGCTGGCTGTGAACCTGGGCGATGGCCCCCATCTTCTTTG 2045
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QY 165 CCTTGGGCTCTACACTGGGAGCTGGCCCTGAACCTGGGCGATGGCCCCCATCTTCTTTG 224
Db 2046 GTGCCCGGCGAGATGGGCTGGG 2066
|||||
QY 225 GTGCCCGACAAATGGGCTGGG 245

RESULT 13
LOCUS HSPBR2 487 bp DNA PRI 20-MAY-1994
DEFINITION Human peripheral benzodiazepine receptor gene, exon 2.
ACCESSION L21952
NID g483403
KEYWORDS benzodiazepine receptor; peripheral benzodiazepine receptor.
SEGMENT 2 of 4
SOURCE Homo sapiens DNA.
ORGANISM Homo sapiens
Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Euthera; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 487)
AUTHORS Lin, D., Chang, Y.J., Strauss, J.F. and Miller, W.L.
TITLE The human peripheral benzodiazepine receptor gene: cloning and
characterization of alternative splicing in normal tissues and in a
patient with congenital lipoid adrenal hyperplasia
Genomics 18, 643-650 (1993)
JOURNAL 94140364
MEDLINE
FEATURES
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1. .487
/organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="placenta"
/tissue_lib="placenta"
166..376
/product="peripheral benzodiazepine receptor"
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Best Local Similarity 100.0%; Pred. No. 8.35e-57;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 272 CCACGGCGAGGGTCTCCGCTGTGTACCGCGCTGTGCAGAGCCCTCTGTGACCCGCCCA 331
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QY 1 CCACGGCGAGGGTCTCCGCTGTGTACCGCGCTGTGCAGAGCCCTCTGTGACCCGCCCA 60
Db 332 CTGGGTGCTGGGCCCTGTCTGGGCGACGCTCTACTCAGCATGGGTA 379
|||||
QY 61 CTGGGTGCTGGGCCCTGTCTGGGCGACGCTCTACTCAGCATGGGTA 108

RESULT 14
LOCUS 166494 7218 bp DNA PAT 23-DEC-1997
DEFINITION Sequence 14 from patent US 5670367.
ACCESSION 166494
NID g2724471
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 7218)
AUTHORS Dorner, F., Scheiflinger, F. and Falkner, F. Gunter.
TITLE Recombinant fowlpox virus
JOURNAL Patent: US 5670367-A 14 23-SEP-1997;
FEATURES
source
1. 7218
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BASE COUNT 1944 a 1491 c 1486 g 1929 t 368 others
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Best Local Similarity 0.3%; Pred. No. 1.90e-08;
Matches 1; Conservative 203; Mismatches 165; Indels 0; Gaps 0;

Db 1067 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1126
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 13 TCTCGCTGTACGCGCGCTGCAGAGCCCTCGTGGCACCGCCCACTGGTGTGGTGG 72
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1127 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1186
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 73 CCTGTCTGGGCACGCTACTACAGCCATGGGTACGGCTCTACCTGTCTGGAAGA 132
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1187 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1246
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 133 GTGGAGGCTTCACAGAGAGCTGTGTTCCCTGGCGCTCTACACTGGGCAGCTGGC 192
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1247 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1306
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 193 CCTGAACGGCATGCGCCGCCATCTCTTGTGGCCGACAAATGGGTGGCGCTTGT 252
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1307 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1366
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 253 GGATCTCTCTGTGTGAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 312
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1367 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1426
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Qy 313 CCGCTGGCGCGCGCGCTGTCTACCCCTACCTGGCTGGCGCTGGCGCTGGCGCTGG 372
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1427 YYYYYYYYG 1435
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 373 CAACACTG 381

RESULT 15
LOCUS CGU12420 1084 bp DNA ROD 14-DEC-1995
DEFINITION Cricetulus griseus mitochondrial benzodiazepine receptor (MBR)
ACCESSION U12420
NID 9529943
KEYWORDS
SOURCE Chinese hamster.
ORGANISM Cricetulus griseus
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Cricetinae; Cricetulus.
REFERENCE 1 (bases 41 to 1029)
AUTHORS Yakovlev,A.G., Ruffo,M., Jurka,J. and Krueger,K.E.
TITLE Comparison of repetitive elements in the third intron of human and
rodent mitochondrial benzodiazepine receptor-encoding genes
JOURNAL Gene 155 (2), 201-205 (1995)
MEDLINE 95237610
REFERENCE 2 (bases 1 to 1084)
AUTHORS Krueger,K.E.
TITLE Direct Submission
JOURNAL Submitted (19-JUL-1994) Karl E. Krueger, Dept. of Cell Biology,
Georgetown University School of Medicine, Washington, DC 20007, USA
FEATURES
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/clone_lib="PCR of genomic DNA"
/cell_line="V79"
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/evidence=experimental
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/codon_start=2
/product="mitochondrial benzodiazepine receptor"
/db_xref="PID:g1039378"

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repeat_region 657..736
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/number=4
/evidence=experimental
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BASE COUNT 253 a 279 c 302 g 250 t
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Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 1 ATGGCCCCCATCTCTTGTGGCCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 41
|||||
Qy 205 ATGGCCCCCATCTCTTGTGGCCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 245

Search completed: Tue Jul 21 15:51:40 1998
Job time : 845 secs.

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Result No.	Query			ID	Description	Pred. No.
	Score	Match	Length			
1	238	36.5	272	Q21195	Human gene signature	3.02e-134
2	44	6.7	91	T31746	Oligonucleotide probe	2.23e-11
C 3	41	6.3	204	1 N81184	Base substituted E.co	1.04e-09
4	40	6.1	91	Q31746	Oligonucleotide probe	3.68e-09
C 5	36	5.5	114	12 Q70465	Generic DNA sequence	5.38e-07
6	36	5.5	204	1 N81184	Base substituted E.co	5.38e-07
7	35	5.4	114	12 Q70469	Generic DNA sequence	1.83e-06
8	34	5.2	114	12 Q70468	Generic DNA sequence	6.18e-05
9	34	5.2	114	12 Q70472	Generic DNA sequence	6.18e-05
10	34	5.2	114	12 Q70455	Generic DNA sequence	6.18e-06
11	34	5.2	114	12 Q70467	Generic DNA sequence	6.18e-06
C 12	34	5.2	114	12 Q70468	Generic DNA sequence	6.18e-06
C 13	34	5.2	114	12 Q70467	Generic DNA sequence	6.18e-06
14	33	5.1	114	12 Q70469	Generic DNA sequence	2.06e-05

Query Match	36.5%	Score 238;	DB 20;	Length 272;
Best Local Similarity	92.3%;	Pred. No. 3,02e-134;		
Matches 251;	Conservative 0;	Mismatches 20;	Indels 1;	Gaps 43
Db	1	gatctcctgctgtagtgagtgaggcgccgcagc-actaccgtgacctgctggtaccaggtgagc	59	
QY	254	GAFTCTCCTGTGTGTAGTGGGGCGGGCAGCACCCATACCGTGGCCCTGGTACCAGGTGACG	313	
Db	60	ccgctggcgccgcctgctctaccctaccctgacctggctggctggcttcgcgaccacactc	119	
QY	314	CCGCTGGCGCGCCGCTGTCTTACCCTTACCTGGCTGGCTGGCCCTTACGACCACTC	373	
Db	120	aactactgcgtatggcgggagacaaccatgctggcatgggggacggcggtgccagagtga	179	
QY	374	AACTACTGCGCTATGGCGGGGAAACCACTATGCTGGCGTGGGGGCGGGCGGTGCCAGAGTGA	433	
Db	180	gtgcccgggccaccaggagantgagtnaccagnaggtggccatnangttntaaIntag	239	
QY	434	GTGCCCGGGCCACCAGGGACTGACGTGCACACGAGGTGCCATCAGCTTGTGTGATGTG	493	
Db	240	tggcgctnangttttaatgaccantgggncgtg	271	
QY	494	TGGCCCGTACGCTTTTCATGACCACTGGGCGCTG	525	

RESULT	2	
ID	Q51746 standard; cDNA; 91 BP.	
AC	Q51746;	
DT	31-MAY-1994 (first entry)	
DE	Oligonucleotide probe MK14-A	
KW	Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;	
KW	ss.	
OS	Synthetic.	
PN	EP-571911-A.	
PD	01-DEC-1993.	
PF	24-MAY-1993; 108325.	
PR	26-MAY-1992; OS-889651.	
PA	(BECT) BECTON DICKINSON CO.	
PI	Shank DD, Spears PA;	
DR	WPI; 93-37884/48.	
PT	New oligo:nucleotide probes specific for Mycobacteria - used for	
PT	detection and amplification of Mycobacteria nucleic acid in	
PT	samples	
PS	Claim 3; Page 14; 23pp; English.	
CC	Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14	
CC	(Q51735). It hybridized to all spp. of mycobacteria tested, but	
CC	cross reacted to a few non-mycobacterial spp. The probe may	
CC	be useful as an initial screen for mycobacterial infection.	
CC	See also Q51735-45 and Q51747-59.	
SC	Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;	

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Query Match          6.7%; Score 44; DB 9; Length 91;
Best Local Similarity 3.8%; Pred. NO. 2.23e-11;
Matches      2; Conservative    46; Mismatches     4; Indels   0; Gaps   0
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Dbb       9 cgssvhsvvvvhhshhvhhvhhvsvvvhhvhhvhhvhhvhyvyvsv 60
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Cp        280 CGCGCCCACTGACAGCAGGAGATCACCAAGGCCAGCCCCATTGTGG 229
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RESULT      3
ID N91164 standard; DNA; 204 BP.
AC N91164;
DT 08-NOV-1990 (first entry)
DE Base substituted E.coli beta-galactosidase alpha-fragment.
KW E.coli beta galactosidase alpha-fragment; base substitutions; ss.
OS Escherichia coli.
FH Key Location/Qualifiers
FT misc_feature 19..69
FT FT /*tag= a
FT /function-multiple cloning site
FT primer_bind 187..204
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FT EP-285123-A. /*tag= b

PN 05-MAY-1988. PD

PF 30-MAR-1988; 105163. PP

PR 03-APR-1987; US-034819. PR

PI (SUSO) SUOMEN SOKERI OY. PI

PI Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen T; PI

DR WPI: 88-279927/40. DR

PT Introducing random point mutations into nucleic acids - PT

PT by prepn of single stranded template, annealing a primer, elongation, PT

PT misincorporation, completion of molecules and screening. PT

PS Disclosure; P: English. PS

CC Random point mutations were introduced into the alpha fragment of CC

CC E.coli beta-galactosidase. The wild type sequence was obtained as a CC

CC single stranded template and an oligonucleotide was hybridised to CC

CC it to generate a popn of DNA molecules which terminate at all CC

CC possible nucleotide positions within a specified region. The CC

CC variable 3' ends generated in this way are used as primers for CC

CC reverse transcriptase. Nucleotides are misincorporated by the CC

CC transcriptase and the molecules are completed to forms that can be CC

CC amplified and then expressed in a suitable host-vector system. CC

CC The sequence covers all 176 diff base substitutions, most of which CC

CC occurred singularly in any given mutant. CC

CC See also P80575. CC

SC Sequence 204 BP; 21 A; 47 C; 17 G; 11 T; 108 Others: SC

Query Match	638	Score 41	DB 1	Length 204
Best Local Similarity	778	pred No. 104	-09	
Matches	8	Conservative	60	Mismatches 35; Indels 1; Gaps 1;
Db	86	ymrtthhyrmrbnvyrdyn-rsdaaawcyeyrravkydcycnecchdhdyvvybbvyn	144	
Cp	190	CAGCTGCCAGTGTAGAGGCCCGAGGGACACACAGCGCTTCTGTGAGCCCTCCACGCTC	131	
Db	145	vhnncncccbnbnhvcnbnhbnhwnayrvhrdarddvocv	188	
Cp	130	TTTCCACAGCAGGTAGAGCGCGTACCCCATGGCTGAGTAGAGCG	87	

RESULT 4

ID Q51746 standard; cDNA; 91 BP.

ID Q51746;

AC 31-MAY-1994 (first entry)

DE Oligonucleotide probe MK14-A

DE Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;

KW ss.

KW Synthetic.

OS EP-571911-A.

PN EP-DEC-1993.

PD 01-DEC-1993.

PF 24-MAY-1993; 108325.

PR 26-MAY-1992; US-889651.

PA (BECT) BECTON DICKINSON CO.

PI Shank DD, Spears PA;

DR WPI: 93-378844/48.

PT New oligo:nucleotide probes specific for Mycobacteria - used for

PT detection and amplification of Mycobacteria nucleic acid in

PT samples

PT Claim 3; Page 14; 23pp; English.

PS Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14

CC (Q51735). It hybridized to all spp. of mycobacteria tested, but

CC cross reacted to a few non-mycobacterial spp. The probe may

CC be useful as an initial screen for mycobacterial infection.

CC See also Q51735-45 and Q51747-59.

CC sequence 91 BP; 5 A; 17 C; 15 G; 4 T;

CC SQ

Query Match	6.1%	Score 40;	DB 9;	Length 91;
Best Local Similarity	10.7%;	Pred. No. 3.68e-09;		
Matches	6;	Conservative	42; Mismatches	8; Indels 0; Gaps 0;
Db	10 gssvhsyvvhvavshhsbhvhvhhvsvvvvhhvvhvhhvhyhvvyavgtcaa	65		
ov	320 gcgcggccgctgcttaccctactcgtgcttgctgcttcacgagcacatcaaa	375		


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RESULT 5
ID Q70465 standard; DNA; 114 BP.
AC Q70465;
DT 05-APR-1995 (first entry)
DE Generic DNA sequence to generate a random TSAR peptide library.
KW TSAR; totally synthetic affinity reagent; synthetic; binding domain;
KW effector domain; concatenated heterofunctional protein; linker;
KW direct; rapid; detection; screening; treatment; generic; ss.
OS Synthetic.
FH Key Location/Qualifiers
FT misc_feature 55..60
FT /tag= a
FT /note= "this sequence represents '2'; 2 can be a
FT sequence of 6, 9 or 12 nucleotides (see
FT comments)"
PN WO9418318-A.
PD 18-AUG-1994.
PF 01-FEB-1994; U00977.
PR 01-FEB-1993; US-013416.
PR 30-DEC-1993; US-176500.
PR 31-JAN-1994; US-189331.
PA (UYNK-) UNIV NORTH CAROLINA.
PI Fowlkes DM, Kay BK;
DR WPI: 94-279739/34.
DR P-PSDB; R65150 and R65151.
PT Identifying proteins or peptide(s) which bind a ligand - by
PT screening a recombinant vector library expressing fusion proteins
PT comprising a binding domain and an effector domain
PS Disclosure; Page 35; 255pp; English.
CC Q70465 is a generic DNA sequence used to generate random TSAR (Totally
CC Synthetic Affinity Reagents) peptides. This generic formula can also be
CC represented as follows: X(NNB)6(TGC)(NNB)14(TGC)(NNB)3Y. X
CC and Y are flanking restriction sites (X is not the same as Y) that are
CC not specified further. Other generic sequences are shown in Q70466-68.
CC Other specific peptides generated by these generic sequences are shown in
CC R65151-54. TSARs are concatenated heterofunctional proteins or peptides,
CC comprising at least two functional regions - a binding domain with
CC affinity for a ligand and a second effector peptide portion that is
CC chemically or biologically active. They may further comprise a linker
CC peptide between the 2 domains. The oligonucleotides are also designed so
CC that the expressed peptide contains 2 or 4 cysteine residues positioned
CC in, or flanking, the unpredicted or variant residues. These residues
CC confer some degree of conformational rigidity to the peptides. The TSARs
CC or compns. comprising a TSAR binding domain can be used in vivo to
CC deliver a chemically or biologically active moiety, eg. metal ion,
CC radioisotope, peptide, toxin or enzyme, to the specific target or on the
CC cell. They can also replace the function of macromolecules, eg.
CC monoclonal or polyclonal antibodies and therefore circumvent the need
CC for complex methods of hybridoma formation or in vivo antibody
CC production. The TSARs are easily characterised and have designed
CC activity allowing direct and rapid detection in a screening process.
SQ Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;

```

```

OS Escherichia coli.
FH Key Location/Qualifiers
FT misc_feature 19..69
FT /tag= a
FT /function-multiple cloning site
FT primer_bind 187..204
FT /tag= b
PN EP-285123-A.
PD 05-MAY-1988.
PF 30-MAR-1988; 105163.
PR 03-APR-1987; US-034819.
PR (SUSO) SUOMEN SOKERI OY.
PI Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen T;
DR WPI: 88-279927/40.
PT Introducing random point mutations into nucleic acids -
PT by prep of single stranded template, annealing a primer, elongation,
PT misincorporation, completion of molecules and screening.
PS Disclosure; p; English.
CC Random point mutations were introduced into the alpha fragment of
CC E.coli beta-galactosidase. The wild type sequence was obtained as a
CC single stranded template and an oligonucleotide was hybridised to
CC it to generate a popn of DNA molecules which terminate at all
CC possible nucleotide positions within a specified region. The
CC variable 3' ends generated in this way are used as primers for
CC reverse transcriptase. Nucleotides are misincorporated by the
CC transcriptase and the molecules are completed to forms that can be
CC amplified and then expressed in a suitable host-vector system.
CC The sequence covers all 176 diff base substitutions, most of which
CC occurred singularly in any given mutant.
CC See also P80375.
SQ Sequence 204 BP; 21 A; 47 C; 17 G; 11 T; 108 Others;
Query Match 5.5%; Score 36; DB 1; Length 204;
Best Local Similarity 15.1%; Pred. No. 5,38e-07;
Matches 16; Conservative 53; Mismatches 35; Indels 2; Gaps 2;
Db 93 hyrrmbvnyrdyn-rsdaaawccrrsvkydcynachddhyv-ybbbvnyvnhnn 150
Qy 19 CTGGTACGCGCCCTCAGAGACCCCTCGTGGCAGCCGCCCTGCTGGCCCTGT 78
Db 151 cncccbnhvhnbnnhwayrhdarrddvhhccvchcgatc 196
Qy 79 CTGGGGCAGCTCTACTCAGCCATGGGTGCTGCTCTCTCTCTCTCTCTCTCT 124
RESULT 7
ID Q70469 standard; DNA; 114 BP.
AC Q70469;
DT 07-APR-1995 (first entry)
DE Generic DNA sequence to generate a random TSAR peptide library.
KW TSAR; totally synthetic affinity reagent; synthetic; binding domain;
KW effector domain; concatenated heterofunctional protein; linker;
KW direct; rapid; detection; screening; treatment; generic; ss.
OS Synthetic.
FH Key Location/Qualifiers
FT misc_feature 55..60
FT /tag= a
FT /note= "this sequence represents '2'; 2 can be a
FT sequence of 6,9 or 12 nucleotides (see
FT comments)"
PN WO9418318-A.
PD 18-AUG-1994.
PF 01-FEB-1994; U00977.
PR 01-FEB-1993; US-013416.
PR 30-DEC-1993; US-176500.
PR 31-JAN-1994; US-189331.
PA (UYNK-) UNIV NORTH CAROLINA.
PI Fowlkes DM, Kay BK;
DR WPI: 94-279739/34.
PT Identifying proteins or peptide(s) which bind a ligand - by
PT screening a recombinant vector library expressing fusion proteins
PT comprising a binding domain and an effector domain
PS Disclosure; Page 35; 255pp; English.

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RESULT      8
ID          Q70468 standard; DNA; 114 BP.
AC          Q70468;
DE          05-APR-1995 (first entry)
DE          Generic DNA sequence to generate a random TSAR petide library.
DE          TSAR: totally synthetic affinity reagent; synthetic; binding domain;
KW          effector domain; concatenated heterofunctional protein; linker;
KW          direct; rapid; detection; screening; treatment; generic; ss.
OS          Synthetic.
FH          Key
FT          Location/Qualifiers
FT          misc_feature
FT          55..60
FT          /*tag= a
FT          /note= "this sequence represents '2'; 2 can be a
FT          sequence of 6, 9 or 12 nucleotides (see
FT          comments)"
FT          WO9418318-A.
PN          18-AUG-1994.
PD          01-FEB-1994; U00977.
PR          01-FEB-1993; US-013416.
PR          30-DEC-1993; US-176500.
PR          31-JAN-1994; US-189331.
PA          (UYNC-) UNIV NORTH CAROLINA.
PI          Fowlkes DM, Kay BK.
PI          WPI; 94-279739/34.
PI          P-PSDB; R65154.
DR          Identifying proteins or peptide(s) which bind a ligand - by
DR          screening a recombinant vector library expressing fusion proteins
PT          comprising a binding domain and an effector domain
PT          Disclosure; page 35; 255pp; English.
PS          Q70468 is a generic DNA sequence used to generate random TSAR (Totally
CC          Synthetic Affinity Reagents) peptides. This generic formula can also be
CC          represented as follows: X(NNB)11(TGC)(NNB)62(NNB)7(TGC)(NNB)110Y. X
CC          and Y are flanking restriction sites (X is not the same as Y) that are
CC          not specified further. Other generic sequences are shown in Q70466-68.
CC          Other specific peptides generated by these generic sequences are shown in

```

R65151-54.	TSARs are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically active.They may further comprise a linker peptide between the 2 domains.The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs or compns. comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process.
Sequence	114 BP; 0 A; 2 C; 2 G; 2 T;
Query Match	5.2%; Score 34; DB 12; Length 114;
Best Local Similarity	2.7%; Pred. No. 6.18e-06;
Matches	3; Conservative 34; Mismatches 75; Indels 0; Gaps 0;
Ddb	3 bnnbnnbnnbnnbnnbnnbnnbnnbntgcnnbnnbnnbnnbnnbnnbnnbnnnnnnnn 62
Qy	16 CGGCTGGTAGCGCGGCTGCAGAGAGCCCTGCTGGACGCCGCCACCTGGTGGGCC 75
Ddb	63 bnnbnnbnnbnnbnnbnnbntgcnnbnnbnnbnnbnnbnnbnnbnnbnnbnnb 114
Qy	76 TGTCTGGGGCGAGCTCTACTCAGCAGTGGGTACGGTCTCTACCTGCTGCTGG 127
RESULT	9
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AC	Q70472;
DT	10-APR-1995 (first entry)
DE	Generic DNA sequence to generate a random TSAR peptide library.
KW	TSAR; totally synthetic affinity reagent; synthetic; binding domain;
KW	effector domain; concatenated heterofunctional protein; linker;
OS	direct; rapid; detection; screening; treatment; generic; ss.
KS	Synthetic.
Key	Location/Qualifiers
FT	misc_feature 55..60
FT	/*tag= a
FT	/note= "encoded by 2"
FN	WO9418318-A.
PT	18-AUG-1994.
PF	01-FEB-1994; U00977.
PR	01-FEB-1993; US-013416.
PR	30-DEC-1993; US-176500.
PR	31-JAN-1994; US-189331.
PR	(UYNK-) UNIV NORTH CAROLINA.
PI	Fowlkes DM, Kay BK;
PI	WPI; 94-279739/34.
DR	P-PSDB; R5838.
PT	Identifying proteins or peptide(s) which bind a ligand - by
PT	screening a recombinant vector library expressing fusion proteins
PT	comprising a binding domain and an effector domain
PS	Disclosure; Page 36; 255pp; English.
CC	Q70472 is a generic DNA sequence used to generate random TSAR (Totally
CC	Synthetic Affinity Reagents) peptides.This generic formula can also be
CC	represented as follows: X(NNB)1(CAC)(NNB)11(CAC)(NNB)(CAC)(NNB)22(NNB)6
CC	-(CAC)(NNB)5(CAC)2(NNB)4. X and Y are flanking restriction sites
CC	(X is not the same as Y) that are not specified further. The peptides
CC	generated by this and other generic sequences (Q70470-73) have invariant
CC	histidine residues incorporated into variant sequences. TSARs are
CC	concatenated heterofunctional proteins or peptides, comprising at least
CC	two functional regions - a binding domain with affinity for a ligand and
CC	a second effector peptide portion that is chemically or biologically
CC	active.They may further comprise a linker peptide between the 2 domains.
CC	the TSARs or compns. comprising a TSAR binding domain can be used in
CC	vivo to deliver a chemically or biologically active moiety, eg. metal
CC	ion, radioisotope, peptide, toxin or enzyme, to the specific target or
CC	on the cell. They can also replace the function of macromolecules, eg.

[illegible]

FH	Key	Location/Qualifiers
FT	misc_feature	55..60
FT		/tag= a
FT		/note= "this sequence represents 'Z'; Z can be a
FT		sequence of 6,9 or 12 nucleotides (see
FT		comments)"
PN		
WT	W09418318-A.	
PD	18-AUG-1994.	
PF	01-FEB-1994;	U00977.
PR	01-FEB-1993;	US-013416.
PR	30-DEC-1993;	US-176500.
PR	31-JAN-1994;	US-189331.
PA	(YINC-) UNIV NORTH CAROLINA.	
PI	Fowlkes DM, Kay BK;	
DR	WPI; 94-279739/34.	
PT	Identifying proteins or peptide(s) which bind a ligand - by	
PT	screening a recombinant vector library expressing fusion proteins	
PT	comprising a binding domain and an effector domain	
PS	Closure; Page 35; 253pp; English.	
CC	CC This generic formula can be represented as follows: X(TGC)(NNB)10-	
CC	CC (TGC)(NNB)6(NNB)2(TGC)(NNB)14(TGC)Y. X and Y are flanking restriction	
CC	CC sites (X is not the same as Y) that are not specified further. This	
CC	CC sequence generates peptides that are cloverleaf in structure. Other	
CC	CC generic sequences are shown in Q70465-68. Other specific peptides	
CC	CC generated by these generic sequences are shown in R65150-54. TSARs are	
CC	CC concatenated heterofunctional proteins or peptides, comprising at least	
CC	CC two functional regions - a binding domain with affinity for a ligand and	
CC	CC a second effector peptide portion that is chemically or biologically	
CC	CC active.They may further comprise a linker peptide between the 2 domains.	
CC	CC The oligonucleotides are also designed so that the expressed peptide	
CC	CC contains 2 or 4 cysteine residues positioned in, or flanking, the	
CC	CC unpredicted or variant residues. These residues confer some degree of	
CC	CC conformational rigidity to the peptides. The TSARs or compans. comprising	
CC	CC a TSAR binding domain can be used in vivo to deliver a chemically or	
CC	CC biologically active moiety, eg. metal ion, radiolotope, peptide, toxin	
CC	CC or enzyme, to the specific target or on the cell. They can also replace	
CC	CC the function of macromolecules, eg. monoclonal or polyclonal antibodies	
CC	CC and therefore circumvent the need for complex methods of hybridoma	
CC	CC formation or in vivo antibody production. The TSARs are easily	
CC	CC characterised and have designed activity allowing direct and rapid	
CC	CC detection in a screening process.	
CC	Sequence 114 BP; 0 A; 4 C; 4 G; 4 T;	
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Query Match 5.1%; Score 33; DB 12; Length 114;		
Best Local Similarity 5.6%; Pred.No. 2.06e-05;		
Matches 6; Conservative 30; Mismatches 71; Indels 0; Gaps 0;		
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Cp	214 GGGGCGCATGCCAGTTTCAGGCGCAGCTGCCAGTGATAGAGCCGACGGGCAACCAGC 155	
Dd	66 btgcnbn 112	
Cp	154 CTTCCTGTGAAGCCCTCCAGCTCTTCCAGACAGGATAGGAGCGGT 108	
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ID	Q70466 standard; DNA; 114 BP.	
AC	Q70466;	
CD	03-APR-1995 (first entry)	
DE	Generic DNA sequence to generate a random TSAR-9 petide library.	
KW	TSAR; totally synthetic affinity reagent; synthetic; binding domain;	
KW	effector domain; concatenated heterofunctional protein; linker;	
KW	direct; rapid; detection; screening; treatment; generic; ss.	
OS	Synthetic.	
FH	Key	Location/Qualifiers
FT	misc_feature	55..60
FT		/tag= a
FT		/note= "this sequence represents 'Z'; Z can be a
FT		sequence of 6, 9 or 12 nucleotides (see
FT		comments)"
PN		
WT	W09418318-A.	

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(TM)

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MParch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Jul 21 15:27:14 1998; MasPar time 36.70 Seconds
953.206 Million cell updates/sec
Tabular output not generated.

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Description: (1-652) from US09047652A.seq
Perfect Score: 652
N.A. Sequence: 1 CCACGGCGAAGGTCTCCGCT.....GTTCTTGGAACATGGAATTT 652
Comp: GGTGCGGCTCCAGAGCGCA.....CAAGAACCTTGACCTTAA

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 104157 seqs, 26825796 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-issued
1:5_COMB 2:PCT9_COMB 3:backfiles

Statistics: Mean 8.113; Variance 4.783; scale 1.696

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	39	6.0	7218	1	US-08-232- Sequence 14, Applicati	2.45e-10
2	36	5.5	215	1	US-08-238- Sequence 5, Applicatio	1.46e-08
3	35	5.4	215	1	US-08-238- Sequence 5, Applicatio	5.58e-08
4	25	3.8	74	2	PCT-US95-1 Sequence 94, Applicati	1.97e-02
5	25	3.8	81	2	PCT-US95-1 Sequence 92, Applicati	1.97e-02
6	24	3.7	74	2	PCT-US95-1 Sequence 94, Applicati	6.50e-02
7	24	3.7	74	2	PCT-US95-1 Sequence 100, Applicat	6.50e-02
8	24	3.7	75	2	PCT-US95-1 Sequence 99, Applicati	6.50e-02
9	24	3.7	81	2	PCT-US95-1 Sequence 92, Applicati	6.50e-02
10	24	3.7	81	2	PCT-US95-1 Sequence 98, Applicati	6.50e-02
11	24	3.7	82	2	PCT-US95-1 Sequence 97, Applicati	6.50e-02
12	23	3.5	66	1	US-08-471- Sequence 144, Applicat	2.10e-01
13	23	3.5	68	1	US-08-471- Sequence 143, Applicat	2.10e-01
14	23	3.5	69	1	US-08-471- Sequence 142, Applicat	2.10e-01
15	23	3.5	74	2	PCT-US95-1 Sequence 100, Applicat	2.10e-01
16	23	3.5	75	2	PCT-US95-1 Sequence 99, Applicati	2.10e-01
17	23	3.5	75	2	PCT-US95-1 Sequence 98, Applicati	2.10e-01
18	23	3.5	82	2	PCT-US95-1 Sequence 97, Applicati	2.10e-01
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20	22	3.4	65	1	US-08-471- Sequence 145, Applicat	6.61e-01

21	22	3.4	66	1	US-08-471- Sequence 144, Applicat	6.61e-01
22	22	3.4	68	1	US-08-471- Sequence 143, Applicat	6.61e-01
23	22	3.4	69	1	US-08-471- Sequence 142, Applicat	6.61e-01
24	22	3.4	242	1	US-08-273- Sequence 1, Applicatio	6.61e-01
25	22	3.4	1995	1	US-08-425- Sequence 3, Applicatio	6.61e-01
26	22	3.4	2256	1	US-08-001- Sequence 1, Applicatio	6.61e-01
27	22	3.4	2256	1	US-07-794- Sequence 1, Applicatio	6.61e-01
28	21	3.2	59	2	PCT-US95-1 Sequence 95, Applicati	2.04e+00
29	21	3.2	59	2	PCT-US95-1 Sequence 93, Applicati	2.04e+00
30	21	3.2	66	2	PCT-US95-1 Sequence 93, Applicati	2.04e+00
31	21	3.2	66	2	PCT-US95-1 Sequence 93, Applicati	2.04e+00
32	21	3.2	108	1	US-08-357- Sequence 2, Applicatio	2.04e+00
33	21	3.2	242	1	US-08-273- Sequence 1, Applicatio	2.04e+00
34	21	3.2	336	1	US-08-248- Sequence 105, Applicat	2.04e+00
35	21	3.2	1441	1	US-08-136- Sequence 18, Applicatio	2.04e+00
36	21	3.2	1838	2	PCT-US93-0 Sequence 85, Applicati	2.04e+00
37	21	3.2	2750	1	US-08-136- Sequence 1, Applicatio	2.04e+00
38	21	3.2	4175	1	US-08-306- Sequence 49, Applicati	2.04e+00
39	21	3.2	4175	2	PCT-US93-0 Sequence 84, Applicati	2.04e+00
40	21	3.2	6063	1	US-08-195- Sequence 4, Applicatio	2.04e+00
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43	20	3.1	84	1	US-08-300- Sequence 25, Applicati	6.11e+00
44	20	3.1	84	2	PCT-US95-1 Sequence 25, Applicati	6.11e+00
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ALIGNMENTS

RESULT 1
ID US-08-232-463-14 STANDARD; DNA; UNC; 7218 BP.
AC xxxxxx
DT
DE Sequence 14, Application US/08232463
CC Sequence 14, Application US/08232463
CC Patent No. 5670367
CC GENERAL INFORMATION:
CC APPLICANT: DORNER, F.
CC APPLICANT: SCHEIFLINGER, F.
CC APPLICANT: FALKNER, F. G.
CC TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
CC NUMBER OF SEQUENCES: 52
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Foley & Lardner
CC STREET: 1800 Diagonal Road, Suite 500
CC CITY: Alexandria
CC STATE: VA
CC COUNTRY: USA
CC ZIP: 22313-0299
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/232,463
CC FILING DATE:
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US/07/935,313
CC FILING DATE:
CC APPLICATION NUMBER: EP 91 114 300.6
CC FILING DATE: 26-AUG-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: BENT, Stephen A.
CC REGISTRATION NUMBER: 29,768
CC REFERENCE/DOCKET NUMBER: 30472/114 IMMU
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (703)836-9300
CC TELEFAX: (703)836-4109
CC TELEX: 899149
CC INFORMATION FOR SEQ ID NO: 14:
CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 7218 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC IMMEDIATE SOURCE:
CC CLONE: PTZgt-Fls
SQ SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER.

Query Match 6.08; Score 39; DB 1; Length 7218;
Best Local Similarity 0.38; Pred. No. 2.45e-10;
Matches 1; Conservative 203; Mismatches 165; Indels 0; Gaps 0;

Db 1067 YY 1126
Qy 13 TCTCCGTGTACCGCGCTGCAGAGCCCTCGTGCACCCGCCACTGGCTGGG 72

Db 1127 YY 1186
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Db 1187 YY 1246
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Db 1247 YY 1306
Qy 193 CCGTGAAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 252

Db 1307 YY 1366
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Db 1367 YY 1426
Qy 313 CCGCTGGCGCGCGCGCGCTGTCTACCCCTACTGCTGGCTGGCTGGCTGGCTGGCTGGCT 372

Db 1427 YYYYYYYYG 1435
Qy 373 CAACTACTG 381

RESULT 2
ID US-08-238-163-5 STANDARD; DNA; UNC; 215 BP.
AC xxxxxx

DE Sequence 5, Application US/08238163
CC Sequence 5, Application US/08238163
CC Patent No. 5569830
CC GENERAL INFORMATION:
CC APPLICANT: BENNETT, Alan
CC APPLICANT: LABAVITCH, John M.
CC APPLICANT: POWELL, Ann
CC APPLICANT: STOTZ, Henrik
CC TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
CC TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
CC NUMBER OF SEQUENCES: 24
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Kourie and Crew
CC STREET: Steuart Street Tower, One Market Plaza
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: US
CC ZIP: 94105-1493
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/238,163
CC FILING DATE: 03-MAY-1994
CC CLASSIFICATION: 800
CC ATTORNEY/AGENT INFORMATION:

CC NAME: Bastian, Kevin L.
CC REGISTRATION NUMBER: 34,774
CC REFERENCE/DOCKET NUMBER: 2307E-540
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 543-9600
CC TELEFAX: (415) 543-5043
CC INFORMATION FOR SEQ ID NO: 5:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 215 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: unknown
CC MOLECULE TYPE: protein
CC FEATURE:
CC NAME/KEY: misc feature
CC LOCATION: 1..215
CC OTHER INFORMATION: /standard_name= "Deduced amino acid
CC OTHER INFORMATION: sequence of PGIP from bean."
SQ SEQUENCE 215 BP; 15 A; 8 C; 25 G; 26 T; 141 OTHER.

Query Match 5.58; Score 36; DB 1; Length 215;
Best Local Similarity 13.48; Pred. No. 1.46e-08;
Matches 28; Conservative 82; Mismatches 98; Indels 1; Gaps 1;

Db 7 SSSVVSRFASNDRAKDGNTSSWTTDCNRTWGVCDTDTTYRVNNDGHNKYSANY 56
Cp 504 CGTGACGGCCACATCACAAAGCGTGATGGCAGCTGCTGGTGCAGCTGCAGTCCCTG 445

Db 67 NYGNNVGAAKHYTHNTVSGADSKVTVDYNSAGTSSNGTDCNRSAGDSY-GSSKT 125
Cp 444 GGCGCGGCGACTACACTCTGGCAGCGCGCTCCGCCAGCCAGCCATGGTGTCCCGCCAT 385

Db 126 AMTSRNRGTGTANNVDSRNGDASVGSCKNTKKHAKNSADGKVGSKNNGDRNNRYGTG 185
Cp 384 ACCAGTAGTGTAGTGTGCTGCTGAAGGCCAGCCAGCCAGGCTAGGGGTAGAGCAGCGG 325

Db 186 KSNVSNCGGKRDVSVYANNKCCGSSC 214
Cp 324 GCGGCCAGCGGCGCTCACCTGGTACCAGGC 296

RESULT 3
ID US-08-238-163-5 STANDARD; DNA; UNC; 215 BP.
AC xxxxxx

DE Sequence 5, Application US/08238163
CC Sequence 5, Application US/08238163
CC Patent No. 5569830
CC GENERAL INFORMATION:
CC APPLICANT: BENNETT, Alan
CC APPLICANT: LABAVITCH, John M.
CC APPLICANT: POWELL, Ann
CC APPLICANT: STOTZ, Henrik
CC TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
CC TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
CC NUMBER OF SEQUENCES: 24
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Kourie and Crew
CC STREET: Steuart Street Tower, One Market Plaza
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: US
CC ZIP: 94105-1493
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/238,163
CC FILING DATE: 03-MAY-1994
CC CLASSIFICATION: 800
CC ATTORNEY/AGENT INFORMATION:

CC	TELEPHONE: (212) 790-9090	
CC	TELEFAX: (212) 869-9741/8864	
CC	TELEX: 66141 PENNIE	
CC	INFORMATION FOR SEQ ID NO: 94:	
CC	SEQUENCE CHARACTERISTICS:	
CC	LENGTH: 74 base pairs	
CC	TYPE: nucleic acid	
CC	STRANDEDNESS: single	
CC	TOPOLOGY: linear	
CC	MOLECULE TYPE: DNA (genomic)	
CC	SEQUENCE 74 BP; 3 A; 4 C; 3 G; 1 T; 63 OTHER.	
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CC	Best Local Similarity	9.98; Pred. No. 1.97e-02;
CC	Matches	7; Conservative 20; Mismatches 44; Indels 0; Gaps 0;
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QY	432 GAGTGCCCGCCACCAGGACGTGCAGCTCACCAGCAGGTGCATCACCCTTGATGT	491
DB	63 BNNBNACGCCA 73	
QY	492 GGTGGCCGTCA 502	
RESULT	5	
ID	PCT-US95-11934-92 STANDARD; DNA; UNC; 81 BP.	
AC	xxxxxx	
DT		
DE	Sequence 92, Application PC/TUS9511934	
CC	Sequence 92, Application PC/TUS9511934	
CC	GENERAL INFORMATION:	
CC	APPLICANT: Cytogen Corporation	
CC	TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From	
CC	TITLE OF INVENTION: Peptide Libraries	
CC	NUMBER OF SEQUENCES: 103	
CC	CORRESPONDENCE ADDRESS:	
CC	ADDRESSEE: Pennie & Edmonds	
CC	STREET: 1155 Avenue of the Americas	
CC	CITY: New York	
CC	STATE: New York	
CC	COUNTRY: USA	
CC	ZIP: 10036	
CC	COMPUTER READABLE FORM:	
CC	MEDIUM TYPE: Floppy disk	
CC	COMPUTER: IBM PC compatible	
CC	OPERATING SYSTEM: PC-DOS/MS-DOS	
CC	SOFTWARE: PatentIn Release #1.0, Version #1.30	
CC	CURRENT APPLICATION DATA:	
CC	APPLICATION NUMBER: PCT/US95/11934	
CC	FILING DATE: 20-SEP-1995	
CC	CLASSIFICATION:	
CC	ATTORNEY/AGENT INFORMATION:	
CC	NAME: Misrock, S. Leslie	
CC	REGISTRATION NUMBER: 18,872	
CC	REFERENCE/DOCKET NUMBER: 1101-196-228	
CC	TELECOMMUNICATION INFORMATION:	
CC	TELEPHONE: (212) 790-9090	
CC	TELEFAX: (212) 869-9741/8864	
CC	TELEX: 66141 PENNIE	
CC	INFORMATION FOR SEQ ID NO: 92:	
CC	SEQUENCE CHARACTERISTICS:	
CC	LENGTH: 81 base pairs	
CC	TYPE: nucleic acid	
CC	STRANDEDNESS: single	
CC	TOPOLOGY: linear	
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CC	SEQUENCE 81 BP; 3 A; 5 C; 6 G; 4 T; 63 OTHER.	
CC	Query Match	3.88; Score 25; DB 2; Length 81;
CC	Best Local Similarity	9.98; Pred. No. 1.97e-02;
CC	Matches	7; Conservative 20; Mismatches 44; Indels 0; Gaps 0;

Db 10 GAGNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNN 69
||| :
Qy 432 GAGTCCCGCCGCGGACTGCGAGTGCACCGAGGTCACATCAGCGTGTGTGATGT 491
:
Db 70 BNNBACGCCA 80
:
Qy 492 GGTGCGCGTCA 502

RESULT 6
ID PCT-US95-11934-94 STANDARD; DNA; UNC; 74 BP.
AC xxxxxx
DT Sequence 94, Application PC/TUS9511934
DE Sequence 94, Application PC/TUS9511934
CC GENERAL INFORMATION:
CC APPLICANT: Cytogen Corporation
CC TITLE OF INVENTION: Antigen Binding Peptides (Abitides) From
CC NUMBER OF SEQUENCES: 103
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Pennie & Edmonds
CC STREET: 1155 Avenue of the Americas
CC CITY: New York
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 10036
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/11934
CC FILING DATE: 20-SEP-1995
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Misrock, S. Leslie
CC REGISTRATION NUMBER: 18,872
CC REFERENCE/DOCKET NUMBER: 1101-196-228
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212) 790-9090
CC TELEFAX: (212) 869-9741/8864
CC TELEX: 66141 PENNIE
CC INFORMATION FOR SEQ ID NO: 94:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 74 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC SEQUENCE 74 BP; 3 A; 4 C; 3 G; 1 T; 63 OTHER.

Query Match 3.7%; Score 24; DB 2; Length 74;
Best Local Similarity 7.7%; Pred. No. 6.50e-02;
Matches 5; Conservative 20; Mismatches 40; Indels 0; Gaps 0;

Db 9 BNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNN 68
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Cp 358 GCGCCAGCCGCGGACTGAGGTAGAGCGGCGCGGCGGCGGCTACCTGTGTACCA 299
:
Db 69 GCGCA 73
:
Cp 298 GCGCA 294

RESULT 7
ID PCT-US95-11934-100 STANDARD; DNA; UNC; 74 BP.
AC xxxxxx
DT Sequence 100, Application PC/TUS9511934
DE Sequence 100, Application PC/TUS9511934
CC GENERAL INFORMATION:
CC APPLICANT: Cytogen Corporation
CC TITLE OF INVENTION: Antigen Binding Peptides (Abitides) From
CC NUMBER OF SEQUENCES: 103
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Pennie & Edmonds
CC STREET: 1155 Avenue of the Americas
CC CITY: New York
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 10036
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: PatentIn Release #1.0, Version #1.30

CC APPLICANT: Cytogen Corporation
CC TITLE OF INVENTION: Antigen Binding Peptides (Abitides) From
CC NUMBER OF SEQUENCES: 103
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Pennie & Edmonds
CC STREET: 1155 Avenue of the Americas
CC CITY: New York
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 10036
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/11934
CC FILING DATE: 20-SEP-1995
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Misrock, S. Leslie
CC REGISTRATION NUMBER: 18,872
CC REFERENCE/DOCKET NUMBER: 1101-196-228
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212) 790-9090
CC TELEFAX: (212) 869-9741/8864
CC TELEX: 66141 PENNIE
CC INFORMATION FOR SEQ ID NO: 100:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 74 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC SEQUENCE 74 BP; 6 A; 6 C; 1 G; 1 T; 60 OTHER.

Query Match 3.7%; Score 24; DB 2; Length 74;
Best Local Similarity 9.1%; Pred. No. 6.50e-02;
Matches 6; Conservative 19; Mismatches 41; Indels 0; Gaps 0;

Db 6 VNNVNNVNNVNNVNNVNNVNNVNNVNNVNNVNNVNNVNNVNNVNN 65
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Cp 554 ACCCTGGCCAGGCGCTGACAGCTAGCAGCGCCAGTGGTATGAAGCGTGACGCGC 495
:
Db 66 ACCACA 71
:
Cp 494 ACCACA 489

RESULT 8
ID PCT-US95-11934-99 STANDARD; DNA; UNC; 75 BP.
AC xxxxxx
DT Sequence 99, Application PC/TUS9511934
DE Sequence 99, Application PC/TUS9511934
CC GENERAL INFORMATION:
CC APPLICANT: Cytogen Corporation
CC TITLE OF INVENTION: Antigen Binding Peptides (Abitides) From
CC NUMBER OF SEQUENCES: 103
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Pennie & Edmonds
CC STREET: 1155 Avenue of the Americas
CC CITY: New York
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 10036
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: PatentIn Release #1.0, Version #1.30

CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
SQ SEQUENCE 81 BP; 3 A; 5 C; 6 G; 4 T; 63 OTHER.

Query Match 3.7%; Score 24; DB 2; Length 81;
Best Local Similarity 7.7%; Pred. No. 6.50e-02;
Matches 5; Conservative 20; Mismatches 40; Indels 0; Gaps 0

Db 16 BNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNA 75
Cp 358 GCCAGCCAGCCAGGTAGGGGTAGACAGCGCGCGCCAGCGGGCTCACCCTGGTACCA 299
Db 76 CGCCA 80
Cp 298 GGCCA 294

RESULT 10
ID PCT-US95-11934-98 STANDARD; DNA; UNC; 81 BP.
AC xxxxxx

DT
CC Sequence 98, Application PC/TUS9511934
CC Sequence 98, Application PC/TUS9511934
CC GENERAL INFORMATION:
CC APPLICANT: Cytogen Corporation
CC TITLE OF INVENTION: Antigen Binding Peptides (AbTides) From
CC TITLE OF INVENTION: Peptide Libraries
CC NUMBER OF SEQUENCES: 103
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Pennie & Edmonds
CC STREET: 1155 Avenue of the Americas
CC CITY: New York
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 10036
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC Compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/11934
CC FILING DATE: 20-SEP-1995
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Mirock, S. Leslie
CC REGISTRATION NUMBER: 18,872
CC REFERENCE/DOCKET NUMBER: 1101-196-228
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212) 790-9090
CC TELEFAX: (212) 869-9741/8864
CC TELEX: 66141 PENNIE
CC INFORMATION FOR SEQ ID NO: 98:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 81 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
SQ SEQUENCE 81 BP; 6 A; 6 C; 4 G; 5 T; 60 OTHER.

Query Match 3.7%; Score 24; DB 2; Length 81;
Best Local Similarity 9.1%; Pred. No. 6.50e-02;
Matches 6; Conservative 19; Mismatches 41; Indels 0; Gaps 0

Db 13 VNNVNNVNNVNNVNNVNNVNNVNNVNNVNNVNNVNNVNNVNNVNNVNN 72
Cp 594 ACCCTGGCCAGGCCCTGTACACTAGCAGCGCCAGTGGTCATGAAGCGTACGCGC 495

Db 73 ACCACA 78
Cp 494 ACCACA 489

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RESULT 11
ID PCT-US95-11934-97 STANDARD; DNA; UNC; 82 BP.
AC xxxxxx
DT
Sequence 97, Application PC/TUS9511934
DE Sequence 97, Application PC/TUS9511934
CC GENERAL INFORMATION:
CC APPLICANT: Cytogen Corporation
CC TITLE OF INVENTION: Antigen Binding Peptides (Abitides) From
CC TITLE OF INVENTION: Peptide Libraries
CC NUMBER OF SEQUENCES: 103
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Pennie & Edmonds
CC STREET: 1155 Avenue of the Americas
CC CITY: New York
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 10036
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/11934
CC FILING DATE: 20-SEP-1995
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Mirock, S. Leslie
CC REGISTRATION NUMBER: 18,872
CC REFERENCE/DOCKET NUMBER: 1101-196-228
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212) 790-9090
CC TELEFAX: (212) 869-9741/8864
CC TELEX: 66141 PENNIE
CC INFORMATION FOR SEQ ID NO: 97:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 82 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC SEQUENCE 82 BP; 1 A; 2 C; 10 G; 8 T; 61 OTHER.
SQ
Query Match 3.78; Score 24; DB 2; Length 82;
Best Local Similarity 10.19; Pred. No. 6.50e-02;
Matches 7; Conservative 19; Mismatches 43; Indels 0; Gaps 0;

Db 7 CTCGAGNNBNBNBNBNBNBNBNBNBNBNBNBNBNBNBNBNBNBNBNBNBN 66
Qy 43 CTCGTGGCACCCGCCACCTGGGTGCTGGGCCCTGCTGGGCACGCTCTACTCAGCCAT 102
: : : : : : : : : : : : : : : : : : : : : : : : : :
Db 67 BNNBNBGG 75
Qy 103 GGGGTACGG 111

RESULT 12
ID US-08-471-052A-144 STANDARD; DNA; UNC; 66 BP.
AC xxxxxx
DT
Sequence 144, Application US/08471052A
DE Sequence 144, Application US/08471052A
CC Patent No. 5625033
CC GENERAL INFORMATION:
CC APPLICANT: Kay, B. K.
CC APPLICANT: Fowlkes, D. M.
CC TITLE OF INVENTION: Totally Synthetic Affinity Reagents
CC NUMBER OF SEQUENCES: 166
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Pennie & Edmonds

```

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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Run on: Tue Jul 21 15:11:50 1998; MasPar time 760.50 Seconds
Tabular output not generated. 1145.170 Million cell updates/sec

Title: >US-09-047-652A-1
Description: (1-652) from US09047652A.seq
Perfect Score: 652
N.A. Sequence: 1 CCACGGCGAAGGTCTCGCT.....GTTCTTGGAAACATGGAATTT 652
Comp: GGTCCGCTCCAGAGCGA.....CAAGAACCTTGACCTTAA

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 1759237 seqs, 667866413 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: emb1-est54
Database: genbank-est106

3:gb_est1 4:gb_est10 5:gb_est11 6:gb_est12 7:gb_est13
8:gb_est14 9:gb_est15 10:gb_est16 11:gb_est17
12:gb_est18 13:gb_est19 14:gb_est20 15:gb_est21
16:gb_est22 17:gb_est23 18:gb_est24 19:gb_est25
20:gb_est26 21:gb_est27 22:gb_est28 23:gb_est29 24:gb_est30
25:gb_est31 26:gb_est32

Statistics: Mean 10.452; Variance 2.420; scale 4.319

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	498	76.4	546	15	AAT24486	ah99h11.s1 Soares NFL
2	493	75.6	572	9	AA587126	nn70b12.s1 NCI_CGAP_La
3	463	71.0	567	13	AA775735	zf31f04.s1 Soares feta
4	459	70.4	563	23	AA161033	zo58e04.s1 Stratagene
5	458	70.2	610	12	AA069479	zm14h11.s1 Stratagene
6	452	69.3	568	10	AA595715	ni46e08.s1 NCI_CGAP_Lu
7	446	68.4	591	11	AA643068	nr95f04.s1 NCI_CGAP_Pr
8	442	67.8	556	8	AA210894	zr90g06.s1 NCI_CGAP_GC
9	437	67.0	541	11	AA479580	zu43a07.s1 Soares ovar
10	425	65.2	541	15	AA478434	ny01b10.s1 NCI_CGAP_GC
11	424	65.0	506	7	AA456315	aa13g10.s1 Soares NHM
12	414	63.5	551	5	AA036726	zk30b07.s1 Soares preg
13	405	62.1	505	16	AA838533	oe39a11.s1 NCI_CGAP_Pr

C	14	399	61.2	543	15	AA805072	ob86c01.s1	NCI_CGAP_GC	0.00e+00
C	15	394	60.4	507	13	AA768741	ob22g01.s1	NCI_CGAP_K1	0.00e+00
C	16	392	60.1	558	11	AA479803	ob23a07.s1	Soares ovar	0.00e+00
C	17	390	59.8	457	7	AA455945	al16e07.s1	Soares NHM	0.00e+00
C	18	386	59.2	505	16	AA768733	oc86h05.s1	NCI_CGAP_GC	0.00e+00
C	19	386	59.2	516	9	AA595368	no36d03.s1	NCI_CGAP_Pr	0.00e+00
C	20	376	57.7	540	12	AA654418	nt03h01.s1	NCI_CGAP_Ly	0.00e+00
C	21	375	57.5	465	11	AA653746	ng63d09.s1	NCI_CGAP_Pr	0.00e+00
C	22	373	57.2	521	9	AA559042	nl11e02.s1	NCI_CGAP_Br	0.00e+00
C	23	364	55.8	504	15	AA805330	oc15c05.s1	NCI_CGAP_GC	0.00e+00
C	24	360	55.2	490	15	AA857072	oe33d06.s1	NCI_CGAP_Pr	0.00e+00
C	25	360	55.2	498	16	AA808022	oc38e02.s1	NCI_CGAP_GC	0.00e+00
C	26	356	54.6	481	15	AA834034	of25e01.s1	NCI_CGAP_K1	0.00e+00
C	27	346	53.1	541	9	AA535901	nf94b05.s1	NCI_CGAP_Co	0.00e+00
C	28	345	52.9	444	22	AA100452	zl81c10.s1	Stratagene	0.00e+00
C	29	342	52.5	401	17	AA904236	oe73g05.s1	NCI_CGAP_Lu	0.00e+00
C	30	341	52.3	419	22	AA09285	z177h01.s1	Stratagene	0.00e+00
C	31	337	51.7	424	23	AA158134	zo43h11.s1	Stratagene	0.00e+00
C	32	320	49.1	495	23	AA158833	zo58e04.s1	Stratagene	0.00e+00
C	33	315	48.3	402	19	N23981	yx71g01.s1	Homo sapien	0.00e+00
C	34	314	48.2	416	22	W44958	zc20g05.s1	Soares sene	0.00e+00
C	35	312	47.9	323	4	AA313263	ES185182	Colon carcin	0.00e+00
C	36	311	47.7	445	16	AA837816	oe39h02.s1	NCI_CGAP_Pr	0.00e+00
C	37	308	47.2	471	22	AA058606	zl86c07.s1	Stratagene	0.00e+00
C	38	308	47.2	541	22	W25523	zb90b12.s1	Soares sene	0.00e+00
C	39	307	47.1	462	20	N63826	za36e09.s1	Homo sapien	0.00e+00
C	40	306	46.9	374	21	W80770	zd90c02.s1	Soares feta	0.00e+00
C	41	306	46.9	578	8	AA210893	zr50g06.s1	NCI_CGAP_GC	0.00e+00
C	42	305	46.8	468	22	AA037186	zc51c06.s1	Soares sene	0.00e+00
C	43	297	45.6	423	22	W70148	zd52g04.s1	Soares feta	0.00e+00
C	44	291	44.6	460	20	N94184	za26e09.s1	Homo sapien	0.00e+00
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ALIGNMENTS

RESULT 1
LOCUS AA724486 546 bp mRNA EST 11-FEB-1998
DEFINITION ah99h11.s1 Soares NFL T GBC S1 Homo sapiens cDNA clone 1327269 3' similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (HUMAN); mRNA sequence.
ACCESSION AA724486
NID g2742193
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 546)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 472.

Location/Qualifiers
1. 546
/organism="Homo sapiens"
/notes=Organ: pooled; Vector: p7T73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung BHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of

FEATURES

source
1. 546
/organism="Homo sapiens"
/notes=Organ: pooled; Vector: p7T73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung BHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of

I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo.
/db_xref="taxon:9606"
/clone="1327269"
/clone_lib="Soares NFL T GBC S1"
/lab_host="DH108"

BASE COUNT 120 a 166 c 166 g 91 t 3 others
ORIGIN

Query Match 76.4%; Score 498; DB 15; Length 546;
Best Local Similarity 98.4%; Pred. No. 0.00e+00;
Matches 503; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 36 AAATTCATGTTCCAGAACATGCTCTAAGCATGCAGAAAGACAGACACTGCTCCCGG 95
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Cp 652 AAATTCATGTTCCAGAACATGCTCTAAGCATGCAGAAAGACAGACACTGCTCCCGG 593
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Db 96 GTGGGGCTCAGGTGGGCCACCTCTGAAGCTCTGCTGACCCCTGGGCCAAGGCCCTGAC 155
|||||
Cp 592 GTGGGGCTCAGGTGGGCCACCTCTGAAGCTCTGCTGACCCCTGGGCCAAGGCCCTGAC 533
|||||
Db 156 AGACTAGCAGGCCCGCAGTGTGTCATGAAGCGGTGACGGCCACACATCACAGCGTGATGGC 215
|||||
Cp 532 AGACTAGCAGGCCCGCAGTGTGTCATGAAGCGGTGACGGCCACACATCACAGCGTGATGGC 473
|||||
Db 216 ACCTGCTGGTCANGCTCAGTCTCTGCTGGGCCGCGCACTCACTCTGGCAGCCGCTCC 275
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Cp 472 ACCTGCTGGTCANGCTCAGTCTCTGCTGGGCCGCGCACTCACTCTGGCAGCCGCTCC 413
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Db 276 CCCAGCCAGCCATGTTGTCGCCCATACGACAGTGTGAGTGTGCTGAGAGGCCAG 335
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Cp 412 CCCAGCCAGCCATGTTGTCGCCCATACGACAGTGTGAGTGTGCTGAGAGGCCAG 353
|||||
Db 336 CCAGCCAGGTAGGGGTAGACAGCGGGGCCAGCGGGCTCACTTGGTACAGGCCAC 395
|||||
Cp 352 CCAGCCAGGTAGGGGTAGACAGCGGGGCCAGCGGGCTCACTTGGTACAGGCCAC 293
|||||
Db 396 GGTAGTGTGNCNGCGCGCCCACTGACGAGGAGATCCACCAAGGCCAGCCCATTTG 455
|||||
Cp 292 GGTAGTGTGCGCGCGCCCACTGACGAGGAGATCCACCAAGGCCAGCCCATTTG 233
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Db 456 TCGGCGACCAAGAGATGGGGGCCATGCCAGTTTACGGGCCAGCTGCCAGGTAGAG 515
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Cp 232 TCGGCGACCAAGAGATGGGGGCCATGCCAGTTTACGGGCCAGCTGCCAGGTAGAG 173
|||||
Db 516 GCCAGGGGAACACAGACCTTCTCTGTGAAG 546
|||||
Cp 172 GCCAGGGGAACACAGACCTTCTCTGTGAAG 142
|||||

RESULT 2
LOCUS AA587126 572 bp mRNA EST 12-SEP-1997
DEFINITION nn70b12.s1 NCI-CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1089215
similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR
(HUMAN);, mRNA sequence.
ACCESSION AA587126
NID 92397940
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 572)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.

Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Stratagene, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 462.

FEATURES
source

Location/Qualifiers
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/note="Organ: larynx; Vector: Bluescript SK-; Site: 1;
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. Larynx. 5' adaptor sequence: 5' GAATTCGCGCAGC
3' 3' adaptor sequence: 5' CTCAGTTTTTTTTTTTTTTT 3'
Average insert size: 0.9 kb."
/db_xref="taxon:9606"
/clone="IMAGE:1089215"
/clone_lib="NCI-CGAP_Lar1"
/tissue_type="larynx"
/lab_host="SOLR (Kanamycin resistant)"
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BASE COUNT 132 a 171 c 173 g 96 t
ORIGIN

Query Match 75.6%; Score 493; DB 9; Length 572;
Best Local Similarity 96.5%; Pred. No. 0.00e+00;
Matches 522; Conservative 0; Mismatches 17; Indels 2; Gaps 2;

Db 34 AAATTCATGTTCCAGAACATGCTCTAAGCATGCAGAAAGACAGACACTGCTCCCGG 93
|||||
Cp 652 AAATTCATGTTCCAGAACATGCTCTAAGCATGCAGAAAGACAGACACTGCTCCCGG 593
|||||
Db 94 GTGGGGCTCAGTGGGGCAACCTCTGAAGCTCTGCTGACCCCTGGGCCAAGGCCCTGAC 153
|||||
Cp 592 GTGGGGCTCAGTGGGGCAACCTCTGAAGCTCTGCTGACCCCTGGGCCAAGGCCCTGAC 533
|||||
Db 154 AGACTAGCAGGCCAGTGTGCTGATGAAGCGTGCAGGCCACACATCACAAAGCGTGATGC 213
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Cp 532 AGACTAGCAGGCCAGTGTGCTGATGAAGCGTGCAGGCCACACATCACAAAGCGTGATGC 473
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Db 214 ACCTGCTGTGACGTGTCAGTCCCTGGTGGCGGGCACTCACTCTGGCAGCGCCGCTCC 273
|||||
Cp 472 ACCTGCTGTGACGTGTCAGTCCCTGGTGGCGGGCACTCACTCTGGCAGCGCCGCTCC 413
|||||
Db 274 CCATGCCAGCCATGTTGTCGCCCATACGAGTAGTTGAGTGTGCTGAGGCCAG 333
|||||
Cp 412 CCATGCCAGCCATGTTGTCGCCCATACGAGTAGTTGAGTGTGCTGAGGCCAG 353
|||||
Db 334 CCAGGCCAGGTAGGGGTAGAGAGCGGGCGCGGCTCACCTGGTACCAGGCCAC 393
|||||
Cp 352 CCAGGCCAGGTAGGGGTAGAGAGCGGGCGCGGCTCACCTGGTACCAGGCCAC 293
|||||
Db 394 GGTAGTGTGACCGCGCCCACTGACAGAGAGATCCACCAAGGCCAGGCCATTTG 453
|||||
Cp 292 GGTAGTGTGCGCGCGCCCACTGACAGAGAGATCCACCAAGGCCAGGCCATTTG 233
|||||
Db 454 TCGGCGACCAAGAAAGATGGGGAGCCATGCCAGTTTCAGGGCAGCTGCACAGGTAGAG 513
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Cp 232 TCGGCGACCAAGAAAGATGGGGAGCCATGCCAGTTTCAGGGCAGCTGCACAGGTAGAG 173
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Db 514 GCCCAGGGAAC-ACAGCCCTTCTCTGTGAAGACTCCAGCTCTTTC-AGACAGGTATGA 571
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Cp 172 GCCCAGGGAACACAGCCCTTCTCTGTGAAGCCTCCAGCTCTTTCAGACAGGTATGA 113
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Db 572 G 572
Cp 112 G 112

RESULT 3

LOCUS AA775735 567 bp mRNA EST 05-FEB-1998
DEFINITION zf31f04.s1 Soares fetal heart NBH19W Homo sapiens cDNA clone
378559 3', similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE
RECEPTOR (HUMAN);, mRNA sequence.

ACCESSION AA775735
NID 92835069
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 567)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,
Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU-NCI human EST Project
Unpublished (1997)

TITLE
JOURNAL
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 487.
Location/Qualifiers
1..567
/organism="Homo sapiens"
/note="Organ: heart; Vector: pT73D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAACTGAGTGGGAGCGCGGCATCTTTTCTTTTCTTTT 3']
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M.Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NBH19W."
/db_xref="GDB:1286815"
/db_xref="taxon:9606"
/clone="378559"
/clone_lib="Soares fetal heart NBH19W"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
126 a 167 c 175 g 98 t 1 others

BASE COUNT 126 a 167 c 175 g 98 t 1 others
ORIGIN

Query Match 71.0%; Score 463; DB 13; Length 567;
Best Local Similarity 96.3%; Pred. No. 0.00e+00;
Matches 522; Conservative 0; Mismatches 12; Indels 8; Gaps 8;

Db 30 AAATTCATGTTCCAGAACATGCTTAAGCATGAGAAAGCAGACATGCTCCCGG 89
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Cp 652 AAATTCATGTTCCAGAACATGCTTAAGCATGAGAAAGCAGACATGCTCCCGG 593
|||||

Db 90 GTGGGGCTCAGGTGGGCGCCACCTCTGAAGCTCTCTGACCCCTGGGCAAGGCGCTGAC 149
|||||
Cp 592 GTGGGGCTCAGGTGGGCGCCACCTCTGAAGCTCTCTGACCCCTGGGCGCCAGGCGCTGAC 533
|||||

Db 150 AGACTAGCAGGCGCCAGTGGTTCATGAAGCGTGACGGCCACCACATCATCAAGCGTGATGCC 209
|||||
Cp 532 AGACTAGCAGGCGCCAGTGGTTCATGAAGCGTGACGGCCACCACATCATCAAGCGTGATGCC 473
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Db 210 ACCTGCTGGTG-AGCTGACGAGCTCTGGTGGGCGGCGGCGACTACTCTGGCAGCGCGCTCC 268
|||||
Cp 472 ACCTGCTGGTGACGTGAGTCCCTGGTGGGCGGCGGCGACTCACTCTGGCAGCGCGCTCC 413
|||||

Db 269 CCCACGCCAGCCATGTTGTTCCCGCCCATACGCAGTAGTTCAGTGTGTCGTGAAGGCCAC 328
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Cp 412 CCCACGCCAGCCATGTTGTTCCCGCCCATACGCAGTAGTTCAGTGTGTCGTGAAGGCCAC 353
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Db 329 CCAGGCTAGTAGGGGTAGACAGCGGGCGGCCAGCGGGCTCACCTGGTACCAGGCCAC 388
|||||
Cp 352 CCAGGCGAGGTAGGGGTAGACAGCGGGCGGCCAGCGGGCTCACCTGGTACCAGGCCAC 293
|||||

Db 389 GGTAGTGTAGCTCCGCCCCCTGACCGAGGAGATCCACCAAGGCCAGCCCATTTG 448
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Cp 292 GGTAGTGGCTGCCCGCCCTGACCGAGGAGATCCACCAAGGCCAGCCCATTTG 233
|||||

Db 449 TCGGGCAC-ANAGAAGATGGGGGCCATGCC-AGTTCCAGGGCCAGCTGCCTAGTGTAGAG 506
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Cp 232 TCGGGCACCAAGAAGATGGGGGCCATGCCAGTTCCAGGGCCAGCTGCCAGGTAGAG 173
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Db 507 GCC-AGAGGAAC-ACAGCCTTCTGTGAAGCCTCC-AGCTCTTC-AGAC-AGGTAGGA 561
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Cp 172 GCCAGGGGAACACAGCCTTCTGTGAAGCCTCCAGCTCTTTCCAGACGAGGTAGGA 113
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Db 562 GC 563
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Cp 112 GC 111

RESULT 4
LOCUS AA161033 563 bp mRNA EST 16-DEC-1996
DEFINITION z058e04.s1 Stratagene pancreas (#937208) Homo sapiens cDNA clone
591102 3', similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE
RECEPTOR (HUMAN);, mRNA sequence.

ACCESSION AA161033
NID g1735356
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 563)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hulman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevisan, E.,
Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
WashU-Merck EST Project
Unpublished (1995)

TITLE
JOURNAL
COMMENT Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40m13 fwd. from Amersham
High quality sequence stop: 425.
Location/Qualifiers
1..563
/organism="Homo sapiens"
/note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Pancreatic adenocarcinoma cell line. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor
sequence: 5' GAATTCGCGACGAG 3' -3' adaptor sequence: 5'
CTCAGATTTTCTTTTCTTTT 3'."
/db_xref="taxon:9606"
/clone="591102"
/clone_lib="Stratagene pancreas (#937208)"
/lab_host="SOLR cells (kanamycin resistant)"
complement(<1..>563)
127 a 168 c 169 g 98 t 1 others

BASE COUNT 127 a 168 c 169 g 98 t 1 others
ORIGIN

NID 92411065
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 568)
 REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert_Strausberg@nih.gov
 Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: Stratagene, Inc., David B. Krizman,
 Ph.D.
 CDNA Library Arraying: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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 Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 265.
 FEATURES
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 Location/Qualifiers
 1..568
 /organism="Homo sapiens"
 /note="Organ: lung; Vector: Bluescript SK-; Site_1: EcoRI;
 Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT.
 Bulk lung tumor. 5' adaptor sequence: 5' GAATTCGCACGAG 3'
 3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'
 Average insert size: 1.1 kb.
 /db_xref="taxon:9606"
 /clone="IMAGE:979910"
 /clone_lib="NCI-CGAP_Lu1"
 /tissue_type="lung tumor"
 /lab_host="SOLR (kanamycin resistant)"
 BASE COUNT 124 a 164 c 165 g 113 t 2 others
 ORIGIN
 Query Match 69.3%; Score 452; DB 10; Length 568;
 Best Local Similarity 96.9%; Pred. No. 0.00e+00;
 Matches 496; Conservative 0; Mismatches 10; Indels 6; Gaps 6;
 Db 53 AAATTCATGTTCCAGAACATGCTCTAAGCATGTCAGAAAGCAGACAGGACACTGCTCCCGG 112
 Cp 652 AAATTCATGTTCCAGAACATGCTCTAAGCATGTCAGAAAGCAGACAGGACACTGCTCCCGG 593
 Db 113 GTGGGGCTCAGTGGGGCCACCTCTGAAGCTCTGCTGACCCCTGGGCCAAGGCCCTGCAC 172
 Cp 592 GTGGGGCTCAGTGGGGCCACCTCTGAAGCTCTGCTGACCCCTGGGCCAAGGCCCTGCAC 533
 Db 173 AGACTAGCAGGCCCGGAGTGGTGCATGAAGCGTGACGGCCACCATCATCAAGCGTGATGGC 232
 Cp 532 AGACTAGCAGGCCCGGAGTGGTGCATGAAGCGTGACGGCCACCATCATCAAGCGTGATGGC 473
 Db 233 ACCTGCTGTGTAGTGCAGTCCCTGTGGGGCCGGGCGGCACTCACTTGGCAGCGCCGCTCC 292
 Cp 472 ACCTGCTGTGTAGTGCAGTCCCTGTGGGGCCGGGCGGCACTCACTTGGCAGCGCCGCTCC 413
 Db 293 CCACGCCAGCCATGGTTGTCCTCCGCCCATACGAGTAGTGTGAGTGGTGGTGAAGGCCAG 352
 Cp 412 CCACGCCAGCCATGGTTGTCCTCCGCCCATACGAGTAGTGTGAGTGGTGGTGAAGGCCAG 353
 Db 353 CCAGCCAGGTTAGGAGCAGCGGGCGGCCAGCGGGCTCACTGGTACCGAGGCCAC 412
 Cp 352 CCAGCCAGGTTAGGAGCAGCGGGCGGCCAGCGGGCTCACTGGTACCGAGGCCAC 293
 Db 413 GGTACTGGNN-CCGCGCGCCCCACTGACCCAGCAGGAGATCCACCAAGGCCGCCCATTTG 471

Cp 292 GGTAGTGGCTGCCGCCCGCCCACTGACCACGAGAGATCCACCAAGGCCCGCCCATTTG 233
 Db 472 TCGGGCACCAAAAGATGGGGGCCCATGCAC-GTTCTAGGCGAGCTGCCAA-TGTAGAG 529
 Cp 232 TCGGGCACCAAAAGATGGGGGCCCATGCCAGTTCAGGCCAGCTGCCAGCTGTAGAG 173
 Db 530 GCCAAGGG-AAC-ACAGC-TTCTCTGTGAAGC 558
 Cp 172 GCCCAGGGGAACACAGCCTTCTCTGTGAAGC 141
 RESULT 7
 LOCUS AA643068 591 bp mRNA EST 27-OCT-1997
 DEFINITION nt95504.s1 NCI-CGAP_Pr25 Homo sapiens CDNA clone IMAGE:1175743
 similar to gb:U12421.cds1 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR
 (HUMAN); mRNA sequence.
 ACCESSION AA643068
 NID 92568286
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 591)
 REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert_Strausberg@nih.gov
 Tissue Procurement: Suzanne L. Topalian, M.D., Robert K. Bright,
 Ph.D.
 CDNA Library Preparation: Stratagene, Inc.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 337.
 FEATURES
 source
 Location/Qualifiers
 1..591
 /organism="Homo sapiens"
 /note="Organ: prostate; Vector: Bluescript SK-; Site_1:
 EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
 Oligo dT. Normal prostate epithelial cell line (HPV
 immortalized). 5' adaptor sequence: 5' GAATTCGCACGAG 3'
 3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'
 Average insert size: 1.1 kb.
 /db_xref="taxon:9606"
 /clone="IMAGE:1175743"
 /clone_lib="NCI-CGAP_Pr25"
 /tissue_type="epithelium (cell line)"
 /lab_host="SOLR (kanamycin resistant)"
 BASE COUNT 131 a 179 c 181 g 97 t 3 others
 ORIGIN
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 Best Local Similarity 95.4%; Pred. No. 0.00e+00;
 Matches 544; Conservative 0; Mismatches 11; Indels 15; Gaps 15;
 Db 28 AAATTCATGTTCCAGAACATGCTCTAAGCATGTCAGAAAGCAGACAGGACACTGCTCCCGG 87
 Cp 652 AAATTCATGTTCCAGAACATGCTCTAAGCATGTCAGAAAGCAGACAGGACACTGCTCCCGG 593
 Db 88 GTGGGGCTCAGTGGGGCCACCTCTGAAGCTCTGCTGACCCCTGGGCCAAGGCCCTGAC 147
 Cp 592 GTGGGGCTCAGTGGGGCCACCTCTGAAGCTCTGCTGACCCCTGGGCCAAGGCCCTGAC 533

Db	148	AGACTAGCAGGCCAGTGGTCTATGAAGCGTGAACGCCACCACTATCAACGCGTGATGCC	207
Cp	532	AGACTAGCAGGCCAGTGGTCTATGAAGCGTGAACGCCACCACTATCAACGCGTGATGCC	473
Db	208	ACCTGCTGGTG-AGCTGCAGTCCCTGGTGGCGGGCAGTCACTCTGGCAGCCGC-GTCC	265
Cp	472	ACCTGCTGGTGACGTGCAGTCCCTGGTGGCGGGCAGTCACTCTGGCAGCCGCCTCC	413
Db	266	CCACAGCCAGCCATGGTTGTCGCCCATACGACAGTAGTGTAGTGTGGTGCAGAGGCCAG	325
Cp	412	CCACAGCCAGCCATGGTTGTCGCCCATACGACAGTAGTGTAGTGTGGTGCAGAGGCCAG	353
Db	326	CCAGGCCAGGTAGGGTAGAGCAGCGGGCGGCAGCGGCTCACTGTGTACAGGCCAC	385
Cp	352	CCAGGCCAGGTAGGGTAGAGCAGCGGGCGGCAGCGGCTCACTGTGTACAGGCCAC	293
Db	386	GGTACTGGNCG-CGCGCCCACTGACACGACGAGATCCACCAAGGCCAGCCCATTTG	444
Cp	292	GGTAGTGGTGGCGCGCCCATGACACGACGAGATCCACCAAGGCCAGCCCATTTG	233
Db	445	TCGGGCAC-AAAGAAGATGGGGGCCATGCC-AGTTTCAGGGCAGCTGCC-AGTGTAGAN	501
Cp	232	TCGGGCACAAAGAAGATGGGGGCCATGCCAGTTTCAGGGCAGCTGCCAGTGTAGAG	173
Db	502	GCC-AGGGGAC-ACAGC-TTCTCTGTGAAGCTCC-AGCTCTTTC-AGAC-AGGTAGGA	555
Cp	172	GCCAGGGGAACACAGCTTCTGTGAAGCTCCAGCTCTTTCAGACACAGGTAGGA	113
Db	556	GC-GTACCC-ATG-CTGAGTAGAGTTGCC	582
Cp	112	GCGTACCCCATGGCTGAGTAGAGCTGCC	83

8

RESULT

LOCUS

DEFINITION

ACCESSION

NID

KEYWORDS

SOURCE

ORGANISM

AA210894

z90g06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:683002 3', similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (HUMAN);, mRNA sequence.

AA210894

g1809540

EST.

human.

Homo sapiens

Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 556)

NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -41m13 fwd. ET from Amersham

High quality sequence stop: 428.

FEATURES

source

1..556

/organism="Homo sapiens"

/note="vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer

[5'-TGGTACCACTCAATGGAGCGCGCTCATTTTTTTTTTTTTTTT-3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: estevan@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 598 Std Error: 0.00
Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 52.

FEATURES

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/organism="Homo sapiens"
/notes="Organ: ovary; Vector: pT73D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGAGCGCGCGGTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Bento Soares and
M. Fatima Bonaldo."
/db_xref="Gene:5940628"
/db_xref="taxon:9606"
/clone="740724"
/clone_lib="Soares ovary tumor NBH07"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
BASE COUNT 111 a 155 c 155 g 119 t 1 others
ORIGIN

Query Match 67.0%; Score 437; DB 11; Length 541;
Best Local Similarity 97.9%; Pred. No. 0.00e+00;
Matches 461; Conservative 0; Mismatches 7; Indels 3; Gaps 3;
Db 73 AAATTCCATGTTCCAGAACATGCTTAAGCATGCAGAAACACAGACACTGCTCCCGG 132
|||||
Cp 652 AAATTCCATGTTCCAGAACATGCTTAAGCATGCAGAAACACAGACACTGCTCCCGG 593
|||||
Db 133 GTGGGGCTCAGGTGGGCGCCACCTCTGAAGCTCTGCTGACCCCTGGGCGAAGGCGCTGCAC 192
|||||
Cp 592 GTGGGGCTCAGGTGGGCGCCACCTCTGAAGCTCTGCTGACCCCTGGGCGAAGGCGCTGCAC 533
|||||
Db 193 AGACTAGCAGCGCCAGTGGTGCATGAAGCGTGACGGCCACACATCACAACGCTGATGGC 252
|||||
Cp 532 AGACTAGCAGCGCCAGTGGTGCATGAAGCGTGACGGCCACACATCACAACGCTGATGGC 473
|||||
Db 253 ACCTGCTGGTGAAGTGCAGTCCCTGTGGGCGCGGCACTCACTCTGGCAGCCCGCTCC 312
|||||
Cp 472 ACCTGCTGGTGCAGTGCAGTCCCTGTGGGCGCGGCACTCACTCTGGCAGCCCGCTCC 413
|||||
Db 313 CCCAGCGCCAGCGTGTGCCGCCATACCGACTAGTGTGAGTGTGTCGCGAAGGCCAG 372
|||||
Cp 412 CCCAGCGCCAGCGTGTGTGCCGCCATACCGACTAGTGTGAGTGTGTCGCGAAGGCCAG 353
|||||
Db 373 CCAGCGCAGGTAGGGTAGACAGCGGGCGCCAGCGGCTCCACCTGTGACCAAGGCCA 432
|||||
Cp 352 CCAGCGCAGGTAGGGTAGACAGCGGGCGCCAGCGGCTC-ACCTGTGACCAAGGCCA 294
|||||
Db 433 CGGTAGTGGCNGC-GCCGCCCTGACACAGCAGAGATCCACCAAGGCCCGCCCAATT 491
|||||
Cp 293 CGGTAGTGGCTGCCGCCCTGACACAGCAGAGATCCACCAAGGCCCGCCCAATT 234
|||||
Db 492 GTCGGGCACCAAGAGATGGGGGCGCATGCC-AGTTCAGGGCGCAGTGC 541
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Cp 233 GTCGGGCACCAAGAGATGGGGGCGCATGCCAGTTCAGGGCGCAGTGC 183
|||||

RESULT 10
LOCUS AA748434 541 bp mRNA EST 18-FEB-1998
DEFINITION ny01b10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1270459

similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR
(HUMAN)), mRNA sequence.
AA748434
92788392
EST.
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 541)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)

ACCESSION
NID
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLES
JOURNAL
COMMENT

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

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Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 358.
Location/Qualifiers

FEATURES

source
1 - 541
/organism="Homo sapiens"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD+),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAAGTGGAGCGCGGTTTTTTTTTTTTTTT-
3']. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
/db_xref="taxon:9606"
/clone="IMAGE:1270459"
/clone_lib="NCI_CGAP_GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
BASE COUNT 120 a 152 c 166 g 100 t 3 others
ORIGIN

Query Match 65.2%; Score 425; DB 15; Length 541;
Best Local Similarity 94.7%; Pred. No. 0.00e+00;
Matches 463; Conservative 0; Mismatches 23; Indels 3; Gaps 3;
Db 50 AAATTCCATGTTCCAGAACATGCTTAAGCATGCAGAAACACAGACACTGCTCCCGG 109
|||||
Cp 652 AAATTCCATGTTCCAGAACATGCTTAAGCATGCAGAAACACAGACACTGCTCCCGG 593
|||||
Db 110 GTGGGGCTCAGGTGGGCGCCACCTCTGAAGCTCTGCTGACCCCTGGGCGAAGGCGCTGCAC 169
|||||
Cp 592 GTGGGGCTCAGGTGGGCGCCACCTCTGAAGCTCTGCTGACCCCTGGGCGAAGGCGCTGCAC 533
|||||
Db 170 AGACTAGCAGCGCCAGTGGTGCATGAAGCGTGACGGCCACACATCACAACGCTGATGGC 229
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Cp 532 AGACTAGCAGCGCCAGTGGTGCATGAAGCGTGACGGCCACACATCACAACGCTGATGGC 473
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Db 230 ACCTGCTGGTGCAGTGCAGTCCCTGTGGGCGCGGCACTCACTCTGGCAGCGCGC-GTCC 288
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Cp 472 ACCTGCTGGTGCAGCTGCAGTCCCTGGTGGGGCGGCATCTACTTGGCAGCGCGCTCC 413
Db 289 CCACGCCAGCCAGTGTGTCCCGCCATACGACAGTAGTGTAGTGTGGTGGCGGAAGGCCAG 348
Cp 412 CCCAGCCAGCCAGTGTGTCCCGCCATACGACAGTAGTGTAGTGTGGTGGTGAAGGCCAG 353
Db 349 CCAGGCCAGGTAGGTAGACAGCGGGCGGCGCCAGCGGTGTGACCTGGTAGCAGGCCA 408
Cp 352 CCAGGCCAGGTAGGTAGACAGCGGGCGGCGCCAGCGGTGTGACCTGGTAGCAGGCCA 294
Db 409 CGGTAGGTGNNCCGGCGCCCTACTCACCAGCAGGAGATTCCACCAAGGCCCGCCAGCCATT 468
Cp 293 CGGTAGGTGCGCGCGCCCTACTCACCAGCAGGAGATCCACCAAGGCCCGCCAGCCATT 234
Db 469 GTTCGGNAGCAAGAAGATGGGGGGCATGAC-ATTAAAGGCAAGTTGCCCGAGGTAGA 527
Cp 233 GTGGGCACCAAGAAGATGGGGGGCATGCCAGTTACAGGCCAGCTGCCCGAGGTAGA 174
Db 528 GGCCAGGG 536
Cp 173 GGCCAGGG 165

RESULT 11
LOCUS AA456315 506 bp mRNA EST 06-JUN-1997
DEFINITION aa13g10.s1 Soares Nhmpu S1 Homo sapiens cDNA clone 813186 3'
similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR
(HUMAN);, mRNA sequence.
ACCESSION AA456315
NID 92179525
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
Homo.
REFERENCE 1 (bases 1 to 506)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lucy,M., Le.N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Scheellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wyllie,T., Waterston,R. and Willson,R.
WashU-Merck EST Project 1997
Unpublished (1997)
TITLE
JOURNAL
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 443.
Location/Qualifiers
1..506
/organism="Homo sapiens"
/note="Organ: mixed (see below); Vector: pT73b-Pac
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NBHM, pregnant uterus
NbHPU, and fetal heart NBH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
/db_xref="taxon:9606"
/clone="813186"
/tissue_type="Pooled human melanocyte, fetal heart, and

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pregnant uterus"
/lab_host="DH10B"
/complement(<1..>506)
/db_xref="GDB:6044096"
BASE COUNT 114 a 150 c 158 g 83 t 1 others
ORIGIN

Query Match 65.0%; Score 424; DB 7; Length 506;
Best Local Similarity 96.9%; Pred. No. 0.00e+00;
Matches 483; Conservative 0; Mismatches 10; Indels 5; Gaps 5;

Db 34 AAATTCCATTTTCAAGAACAATGCTCTTAAGCATGCGAGAAAGCACAGACACTGCTCCCGG 93
Cp 652 AAATTCCATTTTCAAGAACAATGCTCTTAAGCATGCGAGAAAGCACAGACACTGCTCCCGG 593
Db 94 GTGGGGCTCAGTGGGGCAACCTCTGAAGCTCTGTGACCCCTGGGCCAAGCCCTGAC 153
Cp 592 GTGGGGCTCAGTGGGGCAACCTCTGAAGCTCTGTGACCCCTGGGCCAAGCCCTGAC 533
Db 154 AGACTAGCAGGCCAGTGGTGCATGAAGCGTGACGGCCACACATCACAGCGTGTATGGC 213
Cp 532 AGACTAGCAGGCCAGTGGTGCATGAAGCGTGACGGCCACACATCACAGCGTGTATGGC 473
Db 214 ACCTGCTGTGAGGCTGCAGTCCCTGGTGGCGCGGCACACTCTGTGGCAGCCGCTCC 273
Cp 472 ACCTGCTGTGAGGCTGCAGTCCCTGGTGGCGCGGCACACTCTGTGGCAGCCGCTCC 413
Db 274 CCATGCCAGCCATGTTGTCGCCCATACGCGAGTAGTTGAGTGTGGTCCGGAAGGCCAG 333
Cp 412 CCACGCCAGCCATGTTGTCGCCCATACGCGAGTAGTTGAGTGTGGTCCGGAAGGCCAG 353
Db 334 CCAGGCCAGGTAGGGTAGAGCAGGGGGCGGCCAGCGGCTCACCTGGTATCCAGGCCAC 393
Cp 352 CCAGGCCAGGTAGGGTAGAGCAGGGGGCGGCCAGCGGCTCACCTGGTATCCAGGCCAC 293
Db 394 GGTACTGGGN-CCGCGCGCCCTACTGACAGCAGGAGATCCACCAAGGCCAGCC-ATTTC 451
Cp 292 GGTAGTGGCTGCCCGCGCCCTACTGACAGCAGGAGATCCACCAAGGCCAGCCATTTC 233
Db 452 TCGGGCAC-AAAGAAGATGGGGGCCATGCC-AGTTTCAGAGCGAGCTGCC-AGTGTAG 506
Cp 232 TCGGGCACCAAGAAGATGGGGGCCATGCCAGTTTCAGGGCCAGCTGCCCATGTAG 175

RESULT 12
LOCUS AA036726 551 bp mRNA EST 10-MAY-1997
DEFINITION 2k30b07.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone
472021 3' similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE
RECEPTOR (HUMAN);, mRNA sequence.
ACCESSION AA036726
NID 91509983
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
Homo.
REFERENCE 1 (bases 1 to 551)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le.M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E.,
Waterston,R., Williamson,A., Wohldmann,P. and Willson,R.
WashU-Merck EST Project
Unpublished (1995)
TITLE
JOURNAL
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the

```

IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 695 Std Error: 0.00
Seq primer: -40m13 fwd. from Amersham
High quality sequence stop: 321.

FEATURES

source
Location/Qualifiers
1. .551
/organism="Homo sapiens"
/note="Organ: uterus; Vector: p7T73-Pac; Site.1: Not I;
Site.2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5',
AACTGGAAGAATTCGGGGCGGCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p7T73 vector. Library
went through one round of normalization. Library
constructed by M. Fatima Bonaldo."
/db_xref="taxon:9606"
/clone="472021"
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/sex="female"
/dev_stage="adult"
/lab_host="DH108"
complement(<1..>551)
/db_xref="GB:3758023"
BASE COUNT 123 a 160 c 164 g 96 t 8 others
ORIGIN

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Best Local Similarity 93.5%; Pred. No. 0.00e+00;
Matches 491; Conservative 0; Mismatches 24; Indels 10; Gaps 10;
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Cp 652 AAATTCCATGTTCCAAAGATGCTTAAGCATGCAGAAAGCAGACACTGCTCCCGG 593
Db 90 GTGGGGCTCAGGTGGGGCCACCTCTGAAGCTCTGTGACCCCTGGGCCAAGGCTG-GAC 148
Cp 592 GTGGGGCTCAGGTGGGGCCACCTCTGAAGCTCTGTGACCCCTGGGCCAAGGCTGAC 533
Db 149 AGACTAGCAGCCAGTGGTTCATGAAGCTGACGGCCACCATCATCAAGCGTGATGGC 208
Cp 532 AGACTAGCAGCCAGTGGTTCATGAAGCTGACGGCCACCATCATCAAGCGTGATGGC 473
Db 209 ACCTGCTGGT-CAGCTGAGTCCCTGGTGGCCGGCAGTCACTCTGGCAGCCGCTCC 266
Cp 472 ACCTGCTGGTGCAGTCCCTGGTGGCCGGCAGTCACTCTGGCAGCCGCTCC 413
Db 267 CCCAGCCAGCCATGGTGTGCCGCCATACGACAGTGTAGTGTGTGTGTAAGGCCAG 326
Cp 412 CCCAGCCAGCCATGGTGTGCCGCCATACGACAGTGTAGTGTGTGTGTAAGGCCAG 353
Db 327 CCAGCCAGGTGAAGGTAGAGCAGGCGGCGGCGGCGTCACTCTGGCAGCCGCTCC 386
Cp 352 CCAGCCAGGTA-GGGGTAGAGCAGGCGGCGGCGGCGGCGTCACTCTGGTACCAGCCA 294
Db 387 CGGTACTGTGANCAGCCGCTTACACAGCAGGAGATCCACAAAGGCCAGCCATTT 446
Cp 293 CGGTAGTGGTGGCGGCCCTACT-GACCAGAGGAGATCCACCAAGGCCAGCCATTT 235
Db 447 TTGTTCCGGCCACCAAGAAGATGGCGGCCATGCCAGTTTCAGGGCCCAAGTGCATGTN 506
Cp 234 T-GT-CGGGCCACCAAGAAGATGGGGGCCATGCCAGTTTCAGGGCCA-GCTGCCAGT- 179
Db 507 GTAGAGCCAGGGGAACACAGACAGTCTTTTGTGGCCCTTCCA 551
Cp 178 GTAGAGCCAGGGGAACACAGACAGTCTTCTGT-GAAGCCTCCCA 135

RESULT 13
LOCUS AA838533 505 bp mRNA EST 18-MAR-1998
DEFINITION OE39a11.s1 NCI-CGAP_Pr25 Homo sapiens cDNA clone IMAGE:141098
similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR
(HUMAN);, mRNA sequence.

ACCESSION
NID
KEYWORDS
SOURCE
ORGANISM

AA838533
g2913332
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 505)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)

JOURNAL

COMMENT
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Suzanne L. Topalian, M.D., Robert K. Bright,
Ph.D.

cDNA Library Preparation: Stratagene, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution Information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

FEATURES

source
Location/Qualifiers
1. .505
/organism="Homo sapiens"
/note="Organ: prostate; Vector: Bluescript SK-; Site.1:
EcoRI; Site.2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Normal prostate epithelial cell line (Hpv
immortalized). 5' adaptor sequence: 5' GAATTCGGCACGAG 3'
3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTTT 3'
Average insert size: 1.1 kb."
/db_xref="taxon:9606"
/clone="IMAGE:1410908"
/clone_lib="NCI-CGAP_Pr25"
/tissue_type="epithelium (cell line)"
/lab_host="SOLR (kanamycin resistant)".
BASE COUNT 112 a 148 c 156 g 89 t
ORIGIN

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Best Local Similarity 94.9%; Pred. No. 0.00e+00;
Matches 444; Conservative 0; Mismatches 21; Indels 3; Gaps 3;
Db 41 AAATTCCATGTTCCAAAGATGCTTAAGCATGCAGAAAGCAGACACTGCTCCCGG 100
Cp 652 AAATTCCATGTTCCAAAGATGCTTAAGCATGCAGAAAGCAGACACTGCTCCCGG 593
Db 101 GTGGGGCTCAGGTGGGGCCACCTCTGAAGCTGTGTGACCCCTGGGCCAAGGCCCTTGAC 160
Cp 592 GTGGGGCTCAGGTGGGGCCACCTCTGAAGCTGTGTGACCCCTGGGCCAAGGCCCTGAC 533
Db 161 AGACTAGCAGCCAGTGGTTCATGAAGCTGACGGCCACCACATCAAGCGTGATGGC 220
Cp 532 AGACTAGCAGCCAGTGGTTCATGAAGCTGACGGCCACCACATCAAGCGTGATGGC 473
Db 221 ACCTGCTGGTTCAGTGTGACCTGGTGGCGGGCAGTCACTCTGGCAGCGCCGCTCC 280
Cp 472 ACCTGCTGGTTCAGTGTGACCTGGTGGCGGGCAGTCACTCTGGCAGCGCCGCTCC 413
Db 281 CCCAGCCAGCCATGGTGTGCCGCCATACGACAGTGTAGTGTGTGTCGCGAAG-CCAG 339
Cp 412 CCCAGCCAGCCATGGTGTGCCGCCATACGACAGTGTAGTGTGTGTCGCGAAGCCAG 353
Db 340 CCAGGCAGGTAGGGTAGAGAGGGGGGGGGC-ACGGGGCTCACCTGGTACCAGGCCAC 398
Cp 352 CCAGGCAGGTAGGGTAGAGAGGGGGGGGGC-ACGGGGCTCACCTGGTACCAGGCCAC 293

/clone="IMAGE:1324464"
/clone_lib="NCI_CGAP_Kid5"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
BASE COUNT 111 a 144 c 151 g 101 t
ORIGIN

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Best Local Similarity 96.5%; Pred. No. 0.00e+00;
Matches 435; Conservative 0; Mismatches 11; Indels 5; Gaps 5;
Db 53 AAATTCCATGTTCCAAGAACATGCTCTAAGCATGCAGAAACACAGGACACTGCTCCCGG 112
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Cp 652 AAATTCCATGTTCCAAGAACATGCTCTAAGCATGCAGAAACACAGGACACTGCTCCCGG 593
|||||
Db 113 GTGGGGGCTCAGGTGGGCCACCTCTGAAGCTCTGCTGACCCCTGGGCCAAGGCTGTAC 172
|||||
Cp 592 GTGGGGGCTCAGGTGGGCCACCTCTGAAGCTCTGCTGACCCCTGGGCCAAGGCTGTAC 533
|||||
Db 173 AGACTAGCAGGCCAGTGGTGCATGAAAGCGTGACGGCCACACATCACAAGCGTGATGGC 232
|||||
Cp 532 AGACTAGCAGGCCAGTGGTGCATGAAAGCGTGACGGCCACACATCACAAGCGTGATGGC 473
|||||
Db 233 ACCTGCTGGTGAGTCTGCAGTCCCTGTGGGGCCGGGCACTCACTCTGGCAGCCGCGTCC 292
|||||
Cp 472 ACCTGCTGGTGAGTCTGCAGTCCCTGTGGGGCCGGGCACTCACTCTGGCAGCCGCGTCC 413
|||||
Db 293 CCCACGCCAGCCATGGTTGTCCCGCCATACGCAGTAGTTGAGTGTGTCGTAAGGCCAG 352
|||||
Cp 412 CCCACGCCAGCCATGGTTGTCCCGCCATACGCAGTAGTTGAGTGTGTCGTAAGGCCAG 353
|||||
Db 353 CCAGGCCAGGTAGGGGTAGACAGCGGGGCCAGCGGGCTACACCTGGTACCAGGCCA 412
|||||
Cp 352 CCAGGCCAGGTAGGGGTAGACAGCGGGGCCAGCGGGCT-CACCTGGTACCAGGCCA 294
|||||
Db 413 CGGTAGGTGACAC-GCCGCCCCACTGACCAGCAGAGATCCAC-AAGGCC-AGCCCATTT 469
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Cp 293 CGGTAGTGGTGGCCGCCCCCACTGACCAGCAGAGATCCACCAAGGCCAGGCCCATTT 234
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Db 470 GTCGGGCCACCAA-GAAGATGGGGGCCATGC 499
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Cp 233 GTCGGGCCACCAAAGAGATGGGGGCCATGC 203
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Search completed: Tue Jul 21 15:24:46 1998
Job time : 776 secs.

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result No.	Score	Query Match	Length	DB	ID	Description	SUMMARIES	
							Pred.	No.
1	238	36.5	272	20	T22195	Human gene signature	6.34e-134	
2	44	6.7	91	9	Q51746	Oligonucleotide probe	2.41e-11	
3	41	6.3	204	1	N81164	Base substituted E.co	1.11e-09	
4	40	6.1	91	9	Q51746	Oligonucleotide probe	3.94e-09	
5	36	5.5	114	12	Q70465	Generic DNA sequence	5.69e-07	
6	36	5.5	204	1	N81164	Base substituted E.co	5.69e-07	
7	35	5.4	114	12	Q70469	Generic DNA sequence	1.93e-06	
8	34	5.2	114	12	Q70468	Generic DNA sequence	6.48e-06	
9	34	5.2	114	12	Q70472	Generic DNA sequence	6.48e-06	
10	34	5.2	114	12	Q70465	Generic DNA sequence	5.48e-06	
11	34	5.2	114	12	Q70467	Generic DNA sequence	6.48e-06	
12	34	5.2	114	12	Q70468	Generic DNA sequence	6.48e-06	
13	34	5.2	114	12	Q70467	Generic DNA sequence	6.48e-06	
14	33	5.1	114	12	Q70469	Generic DNA sequence	2.16e-05	

ALIGNMENTS

RESULT 1

T22195	standard; cDNA to mRNA; 272 BP.
T22195:	
AC	27-AUG-1996 (first entry)
DE	Human gene signature HUNG03766.
DE	Gene signature; messenger RNA; mRNA; r
DE	human; cloning; mapping; non-biased li
KKW	cell typing; abnormal cell function; s
OS	Homo sapiens.
OS	W09514772-A1.
PN	01-JUN-1995.
PN	11-NOV-1994; J01916.
PF	12-NOV-1993; JP-355504.
PR	(MATS/) MATSUBARA K.
PR	(OKUB/) OKUBO K.
PPA	Matsubara K, Okubo K;
PPI	WPI; 95-206931/27.
PPI	Identifying gene signatures in 3'-dire
DR	for diagnosis of abnormal cell functio
PPT	reflects relative abundance of correspo
PPT	tissues
PPT	Claim 1; Page 1088; 2245pp; Japanese.
PCS	A single-stranded DNA (or its compleme
PCS	double-stranded DNA) which comprises o
CCC	given in T19001-T26937 and which is cla
CCC	human genomic DNA, cDNA or mRNA is cla
CCC	sequences were obtained from 3'-direct
CCC	from various human tissues; synthesis
CCC	3'-end of mRNA by using poly(T) as the
CCC	untranslated sequence is unique to a p
CCC	all the 3'-oriented cDNAs hybridize wi
CCC	is constructed so as to reflect accurat
CCC	different mRNAs in the particular tiss
CCC	The appearance frequency of a given GS
CCC	determined (esp. using primers and pro
CCC	sequences) as a means of diagnosing ab
CCC	recognising different cell types.
CSO	Sequence 272 BP; 43 A; 78 C;


```

RESULT 5
ID Q70465 standard; DNA; 114 BP.
AC Q70465;
DT 05-APR-1995 (first entry)
DE Generic DNA sequence to generate a random TSAR peptide library.
KW TSAR; totally synthetic affinity reagent; synthetic; binding domain;
KW effector domain; concatenated heterofunctional protein; linker;
KW direct; rapid; detection; screening; treatment; generic; ss.
OS Synthetic.
FH Key Location/Qualifiers
FT misc_feature 55..60
FT /*tag= a
FT /note= "this sequence represents 'Z'; Z can be a
FT sequence of 6, 9 or 12 nucleotides (see
FT comments)"
FN WO9418318-A.
PD 18-AUG-1994.
PF 01-FEB-1994; U00977.
PR 01-FEB-1993; US-013416.
PR 30-DEC-1993; US-176500.
PR 31-JAN-1994; US-189331.
PA (UYNC-) UNIV NORTH CAROLINA.
PI Fowlkes DM, Kay BK;
DR WPI; 94-279739/34.
DR P-PSDB; R65150 and R65151.
DR Identifying proteins or peptide(s) which bind a ligand - by
PT screening a recombinant vector library expressing fusion proteins
PT comprising a binding domain and an effector domain
PS Disclosure; Page 35; 255pp; English.
CC Q70465 is a generic DNA sequence used to generate random TSAR (Totally
CC Synthetic Affinity Reagents) peptides. This generic formula can also be
CC represented as follows: X(NNB)6(TGC)(NNB)14(TGC)(NNB)3Y. X
CC and Y are flanking restriction sites (X is not the same as Y) that are
CC not specified further. Other generic sequences are shown in Q70466-68.
CC Other specific peptides generated by these generic sequences are shown in
CC R65151-54. TSARs are concatenated heterofunctional proteins or peptides,
CC comprising at least two functional regions - a binding domain with
CC affinity for a ligand and a second effector peptide portion that is
CC chemically or biologically active. They may further comprise a linker
CC peptide between the 2 domains. The oligonucleotides are also designed so
CC that the expressed peptide contains 2 or 4 cysteine residues positioned
CC in, or flanking, the unpredicted or variant residues. These residues
CC confer some degree of conformational rigidity to the peptides. The TSARs
CC or compsns. comprising a TSAR binding domain can be used in vivo to
CC deliver a chemically or biologically active moiety, eg. metal ion,
CC radioisotope, peptide, toxin or enzyme, to the specific target or on the
CC cell. They can also replace the function of macromolecules, eg.
CC monoclonal or polyclonal antibodies and therefore circumvent the need
CC for complex methods of hybridoma formation or in vivo antibody
CC production. The TSARs are easily characterised and have designed
CC activity allowing direct and rapid detection in a screening process.
SQ Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;

Query Match 5.5%; Score 36; DB 12; Length 114;
Best Local Similarity 4.5%; Pred. No. 5.68e-07;
Matches 5; Conservative 33; Mismatches 74; Indels 0; Gaps 0;

Db 3 bnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnnn 62
Cp 151 CTCTGTGAAGCTCCACCGCTTTTCACAGCACGAGGAGCGGTACCCCGCTGGTGAGTA 92
Db 63 bnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnb 114
Cp 91 GAGCGTGCCCGACAGAGGCCGACCGACCGAGTGGGGCGGTGCCACGAGGGC 40

RESULT 6
ID N81164 standard; DNA; 204 BP.
AC N81164;
DT 08-NOV-1990 (first entry)
DE Base substituted E.coli beta-galactosidase alpha-fragment.
KW E.coli beta galactosidase alpha-fragment; base substitutions; ss.

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OS Escherichia coli.
FH Key Location/Qualifiers
FT misc_feature 19..69
FT /*tag= a
FT /function= multiple cloning site
FT primer_bind 187..204
FT /*tag= b
FN EP-285123-A.
PD 05-MAY-1988.
PF 30-MAR-1988; 105163.
PR 03-APR-1987; US-034819.
PR (SUSO) SUOMEN SOKERI OY.
PI Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen T;
DR WPI; 88-279927/40.
DR Introducing random point mutations into nucleic acids -
PT by prepn of single stranded template, annealing a primer, elongation,
PT misincorporation, completion of molecules and screening.
PS Disclosure; p; English.
CC Random point mutations were introduced into the alpha fragment of
CC E.coli beta-galactosidase. The wild type sequence was obtained as a
CC single stranded template and an oligonucleotide was hybridised to
CC it to generate a popn of DNA molecules which terminate at all
CC possible nucleotide positions within a specified region. The
CC variable 3' ends generated in this way are used as primers for
CC reverse transcriptase. Nucleotides are misincorporated by the
CC transcriptase and the molecules are completed to forms that can be
CC amplified and then expressed in a suitable host-vector system.
CC The sequence covers all 176 diff base substitutions, most of which
CC occurred singularly in any given mutant.
CC See also P80575.
SQ Sequence 204 BP; 21 A; 47 C; 17 G; 11 T; 108 Others;

Query Match 5.5%; Score 36; DB 1; Length 204;
Best Local Similarity 15.1%; Pred. No. 5.68e-07;
Matches 16; Conservative 53; Mismatches 35; Indels 2; Gaps 2;

Db 93 hyrrmbnrvrdyn-rsdaawycrrsvkydcynachddhdy-ybbvynvnhnn 150
Qy 19 CTGTGACCGCGCTCGAGAGAGCCCTGTCGACCGCCGACCTGGTGGCCCTGT 78
Db 151 cnccebnnhcnvbnbnrwnvayrhdrrdvhccvchccgac 196
Qy 79 CTGGGGCAGCGCTCTACTACGACGATGGGGTACGGCTCTACCTGGTC 124

RESULT 7
ID Q70469 standard; DNA; 114 BP.
AC Q70469;
DT 07-APR-1995 (first entry)
DE Generic DNA sequence to generate a random TSAR peptide library.
KW TSAR; totally synthetic affinity reagent; synthetic; binding domain;
KW effector domain; concatenated heterofunctional protein; linker;
KW direct; rapid; detection; screening; treatment; generic; ss.
OS Synthetic.
FH Key Location/Qualifiers
FT misc_feature 55..60
FT /*tag= a
FT /note= "this sequence represents 'Z'; Z can be a
FT sequence of 6, 9 or 12 nucleotides (see
FT comments)"
FN WO9418318-A.
PD 18-AUG-1994.
PF 01-FEB-1994; U00977.
PR 01-FEB-1993; US-013416.
PR 30-DEC-1993; US-176500.
PR 31-JAN-1994; US-189331.
PA (UYNC-) UNIV NORTH CAROLINA.
PI Fowlkes DM, Kay BK;
DR WPI; 94-279739/34.
DR Identifying proteins or peptide(s) which bind a ligand - by
PT screening a recombinant vector library expressing fusion proteins
PT comprising a binding domain and an effector domain
PS Disclosure; Page 35; 255pp; English.

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(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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Distribution rights by Oxford Molecular Ltd
MPsrch_n n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Tue Jul 21 16:07:26 1998; MapPar time 36.85 Seconds
Tabular output not generated. 949.152 Million cell updates/sec
Title: >US-09-047-652A-2
Description: (1-652) from US09047652A.seq
Perfect Score: 652
N.A. Sequence: 1 CCACGGCGGAGGCTCCGCT.....GTTCTTGGAACTGGAATTT 652
Comp: GGTCCGCTCCACGAGCGA.....CAAGAACCTGTACCTTAA

Scoring table: TABLE default
Gap 6
Nmatch STD : Dbase 0; Query 0
Searched: 104157 seqs, 26825796 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: n-issued
1:5_COMB 2: PCT9_COMB 3: backfiles
Statistics: Mean 8.110; Variance 4.794; scale 1.692
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES							
Result No.	Score	Query Match	Length	ID	Description	Pred. No.	
1	39	6.0	7218	1	US-08-232-Sequence 14, Applicati	2.64e-10	
2	36	5.5	215	1	US-08-238-Sequence 5, Applicatio	1.55e-08	
3	35	5.4	215	1	US-08-238-Sequence 5, Applicatio	5.93e-08	
4	25	3.8	74	2	PCT-US95-1Sequence 94, Applicati	2.03e-02	
5	25	3.8	81	2	PCT-US95-1Sequence 92, Applicati	2.03e-02	
6	24	3.7	74	2	PCT-US95-1Sequence 94, Applicati	6.88e-02	
7	24	3.7	74	2	PCT-US95-1Sequence 100, Applicat	6.88e-02	
8	24	3.7	75	2	PCT-US95-1Sequence 99, Applicati	6.68e-02	
9	24	3.7	81	2	PCT-US95-1Sequence 98, Applicati	6.68e-02	
10	24	3.7	82	2	PCT-US95-1Sequence 97, Applicati	6.68e-02	
11	24	3.7	66	1	US-08-471-Sequence 143, Applicat	2.15e-01	
12	23	3.5	68	1	US-08-471-Sequence 142, Applicat	2.15e-01	
13	23	3.5	69	1	US-08-471-Sequence 100, Applicat	2.15e-01	
14	23	3.5	74	2	PCT-US95-1Sequence 99, Applicati	2.15e-01	
15	23	3.5	75	2	PCT-US95-1Sequence 98, Applicati	2.15e-01	
16	23	3.5	81	2	PCT-US95-1Sequence 97, Applicati	2.15e-01	
17	23	3.5	82	2	PCT-US95-1Sequence 145, Applicat	6.76e-01	
18	23	3.5	65	1	US-08-471-Sequence 145, Applicat	6.76e-01	
19	22	3.4	65	1	US-08-471-Sequence 145, Applicat	6.76e-01	
20	22	3.4	65	1	US-08-471-Sequence 145, Applicat	6.76e-01	

21	22	3.4	66	1	US-08-471-Sequence 144, Applicat	6.76e-01
22	22	3.4	68	1	US-08-471-Sequence 143, Applicat	6.76e-01
23	22	3.4	69	1	US-08-471-Sequence 142, Applicat	6.76e-01
24	22	3.4	242	1	US-08-273-Sequence 1, Applicatio	6.76e-01
25	22	3.4	1995	1	US-08-425-Sequence 3, Applicatio	6.76e-01
26	22	3.4	2256	1	US-08-001-Sequence 1, Applicatio	6.76e-01
27	22	3.4	2256	1	US-07-794-Sequence 1, Applicatio	6.76e-01
28	21	3.2	59	2	PCT-US95-1Sequence 95, Applicati	2.08e+00
29	21	3.2	59	2	PCT-US95-1Sequence 95, Applicati	2.08e+00
30	21	3.2	66	2	PCT-US95-1Sequence 93, Applicati	2.08e+00
31	21	3.2	66	2	PCT-US95-1Sequence 93, Applicati	2.08e+00
32	21	3.2	108	1	US-08-357-Sequence 2, Applicatio	2.08e+00
33	21	3.2	242	1	US-08-273-Sequence 1, Applicatio	2.08e+00
34	21	3.2	336	1	US-08-248-Sequence 105, Applicat	2.08e+00
35	21	3.2	1441	1	US-08-136-Sequence 18, Applicati	2.08e+00
36	21	3.2	1838	2	PCT-US93-0Sequence 85, Applicati	2.08e+00
37	21	3.2	2750	1	US-08-136-Sequence 1, Applicatio	2.08e+00
38	21	3.2	4175	1	US-08-306-Sequence 49, Applicati	2.08e+00
39	21	3.2	4175	2	PCT-US93-0Sequence 84, Applicati	2.08e+00
40	21	3.2	6063	1	US-08-195-Sequence 4, Applicatio	2.08e+00
41	21	3.2	11558	2	PCT-US93-0Sequence 23, Applicati	2.08e+00
42	20	3.1	84	1	US-08-133-Sequence 120, Applicati	6.21e+00
43	20	3.1	84	1	US-08-300-Sequence 25, Applicati	6.21e+00
44	20	3.1	84	2	PCT-US95-1Sequence 25, Applicati	6.21e+00
45	20	3.1	5399	1	US-08-368-Sequence 9, Applicatio	6.21e+00

ALIGNMENTS

RESULT 1
ID US-08-232-463-14 STANDARD; DNA; UNC; 7218 BP.
AC xxxxxx
DE Sequence 14, Application US/08232463
CC Sequence 14, Application US/08232463
CC Patent No. 5670367
CC GENERAL INFORMATION:
CC APPLICANT: DORNER, F.
CC APPLICANT: SCHEIFLINGER, F.
CC APPLICANT: FALKNER, F. G.
CC TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
CC NUMBER OF SEQUENCES: 52
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Foley & Lardner
CC STREET: 1800 Diagonal Road, Suite 500
CC CITY: Alexandria
CC STATE: VA
CC COUNTRY: USA
CC ZIP: 22313-0299
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/232,463
CC FILING DATE:
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US/07/935,313
CC FILING DATE:
CC APPLICATION NUMBER: EP 91 114 300.6
CC FILING DATE: 26-AUG-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: BENT, Stephen A.
CC REGISTRATION NUMBER: 29,768
CC REFERENCE/DOCKET NUMBER: 30472/114 IMMU
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (703)836-9300
CC TELEFAX: (703)683-4109
CC TELEX: 899149
CC INFORMATION FOR SEQ ID NO: 14:
CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 7218 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC IMMEDIATE SOURCE:
CC CLONE: pTgpt-F1s
CC SEQUENCE 7218 BP, 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER.

Query Match 6.0%; Score 39; DB 1; Length 7218;
Best Local Similarity 0.3%; Pred. No. 2.64e-10;
Matches 1; Conservative 203; Mismatches 165; Indels 0; Gaps 0;

Db 1067 YY 1126
QY 13 TCTCGCTGGTACGGCGCTCAGAGAGCCCTCGTGGCACCCGCCACTGGGTGCTGGG 72
Db 1127 YY 1186
QY 73 CCTGTCTGGGCGAGCTCTACTAGCATGGGTACGGCTCTACCTGGCTGGAAGA 132
Db 1187 YY 1246
QY 133 GCTGGAGGCTTCACAGAGAGGCTGTGTTCCCTGGGCTCTACACTGGGCGAGTGGC 192
Db 1247 YY 1306
QY 193 CTTGAAGTGGGCGATGGCGCCCATCTCTTTGGTGGCCGACAAATGGGCTGGCTTGGT 252
Db 1307 YY 1366
QY 253 GGATCTCTGTGTCAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 312
Db 1367 YY 1426
QY 313 CCGCTGGCGCGCGCGCTCTACCCCTACTGCGCTGCGCTGCGCTGCGCTGCGCT 372
Db 1427 YYYYYYYG 1435
QY 373 CAACTACTG 381

RESULT 2
ID US-08-238-163-5 STANDARD; DNA; UNC; 215 BP.
AC xxxxxx
DE Sequence 5, Application US/08238163
CC Sequence 5, Application US/08238163
CC Patent No. 5569830
CC GENERAL INFORMATION:
CC APPLICANT: BENNETT, Alan
CC APPLICANT: LABAVITCH, John M.
CC APPLICANT: POWELL, Ann
CC APPLICANT: STOTZ, Henrik
CC TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
CC TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
CC NUMBER OF SEQUENCES: 24
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Kourie and Crew
CC STREET: Steuart Street Tower, One Market Plaza
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: US
CC ZIP: 94105-1493
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/238.163
CC FILING DATE: 03-MAY-1994
CC CLASSIFICATION: 800
CC ATTORNEY/AGENT INFORMATION:

CC NAME: Bastian, Kevin L.
CC REGISTRATION NUMBER: 34,774
CC REFERENCE/DOCKET NUMBER: 2307E-540
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 543-9600
CC TELEFAX: (415) 543-5043
CC INFORMATION FOR SEQ ID NO: 5:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 215 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: unknown
CC MOLECULE TYPE: protein
CC FEATURE:
CC NAME/KEY: misc_feature
CC LOCATION: 1..215
CC OTHER INFORMATION: /standard_name= "Deduced amino acid
CC OTHER INFORMATION: sequence of PCIP from bean."
CC SEQUENCE 215 BP; 15 A; 8 C; 25 G; 26 T; 141 OTHER.

Query Match 5.5%; Score 36; DB 1; Length 215;
Best Local Similarity 13.4%; Pred. No. 1.55e-08;
Matches 28; Conservative 82; Mismatches 98; Indels 1; Gaps 1;

Db 7 SSSVSVRTASCKNDKAKKDGNTTSSWTTCCNRTWGVCDTDTTYRVNDSGHNKYSANY 66
Cp 504 CGTGACGGCGCCACATCACAGCGTGATGGCACCTGCTGGTGCAGCTGCAGTCCCTGGT 445
Db 67 NYGNNVGAAKTHYTHNTVSGADSKTVTDSYNASGTSSSNGGTDGNSGADSY-GSSKT 125
Cp 444 GGGCGGGCGACTCACTCTGGACGGCGGCTCCCGCCAGCCAGCCATGTTGTCGCCCAT 385
Db 126 AMTSRNRRTGKTANNVDSRNMGDASVGSNDRTKKHAKNSADGKVGSKNNGDRNNRYGTG 185
Cp 384 AGCAGTAGTTAGTGTGGTGTGTAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 325
Db 186 KSNVSNCGGKRDVSSYANNKCGSSC 214
Cp 324 GCGGCCAGCGGCTCACCTGGTACCAGCG 296

RESULT 3
ID US-08-238-163-5 STANDARD; DNA; UNC; 215 BP.
AC xxxxxx
DE Sequence 5, Application US/08238163
CC Sequence 5, Application US/08238163
CC Patent No. 5569830
CC GENERAL INFORMATION:
CC APPLICANT: BENNETT, Alan
CC APPLICANT: LABAVITCH, John M.
CC APPLICANT: POWELL, Ann
CC APPLICANT: STOTZ, Henrik
CC TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
CC TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
CC NUMBER OF SEQUENCES: 24
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Kourie and Crew
CC STREET: Steuart Street Tower, One Market Plaza
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: US
CC ZIP: 94105-1493
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/238.163
CC FILING DATE: 03-MAY-1994
CC CLASSIFICATION: 800
CC ATTORNEY/AGENT INFORMATION:

```
CC NAME: Bastian, Kevin L.
CC REGISTRATION NUMBER: 34,774
CC REFERENCE/DOCKET NUMBER: 2307B-540
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 543-9600
CC TELEFAX: (415) 543-5043
CC INFORMATION FOR SEQ ID NO: 5:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 215 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC MOLECULE TYPE: protein
CC TOPOLOGY: unknown
CC NAME/KEY: misc_feature
CC LOCATION: 1..215
CC OTHER INFORMATION: /standard_name= "deduced amino acid
CC OTHER INFORMATION: sequence of PGIP from bean."
CC SEQUENCE 215 BP; 15 A; 8 C; 25 G; 26 T; 141 OTHER.
SO

Query Match 5.4%; Score 35; DB 1; Length 215;
Best Local Similarity 12.4%; Pred. No. 5,93e-08;
Matches 25; Conservative 81; Mismatches 95; Indels 1; Gaps 1;

Db 9 SSVSVRTASCHNDKAKKDGNTSSWTTDCNRTWGVCDTDTTYRVNDSGNHNYSSANYNY 68
Qy 304 CCAGGTGAGCCCGCTGGCGCCGCGCTCTCTACCCCTACCTGCGCTGGCTTTCAC 363
Db 69 GGNVNGAKTHYHTNVSG-ADSKVTDSYNASGTSSTSSNGTGNRSGADSYGSSKTAM 127
Qy 364 GACCACACTCAACTACTCGTACTGCGGGGACCAACCATGGCTGGGGACGCGGCT 423
Db 128 TSNRTGTANNVDSNRNGDASVSGSDKTRKHAKNASDGVKGNKNNDRNNRYGTGTS 187
Qy 424 GCCAGGTGAGTGGCCGCCACAGGAGTGCAGCTGCACAGGAGTGCATCACGCT 483
Db 188 NVNNCGGKRVSSYANNKC 209
Qy 484 TGTGTGTGGTGGCGGTCAACGC 505

RESULT 4
ID PCT-US95-11934-94 STANDARD; DNA; UNC; 74 BP.
AC xxxxxx
DE Sequence 94, Application PC/TUS9511934
CC Sequence 94, Application PC/TUS9511934
CC GENERAL INFORMATION:
CC APPLICANT: CytoGen Corporation
CC TITLE OF INVENTION: Antigen Binding Peptides (Ablides) From
CC TITLE OF INVENTION: Peptide Libraries
CC NUMBER OF SEQUENCES: 103
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Pennie & Edmonds
CC STREET: 1155 Avenue of the Americas
CC CITY: New York
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 10036
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent in Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/11934
CC FILING DATE: 20-SEP-1995
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Mistrock, S. Leslie
CC REGISTRATION NUMBER: 18,872
CC REFERENCE/DOCKET NUMBER: 1101-196-228
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212) 790-9090
CC TELEFAX: (212) 869-9741/8864
CC TELEX: 66141 PENNIE
CC INFORMATION FOR SEQ ID NO: 92:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 81 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC SEQUENCE 81 BP; 3 A; 5 C; 6 G; 4 T; 63 OTHER.
SO

Query Match 3.8%; Score 25; DB 2; Length 81;
Best Local Similarity 9.9%; Pred. No. 2.03e-02;
Matches 7; Conservative 20; Mismatches 44; Indels 0; Gaps 0;

CC TELEPHONE: (212) 790-9090
CC TELEFAX: (212) 869-9741/8864
CC TELEX: 66141 PENNIE
CC INFORMATION FOR SEQ ID NO: 94:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 74 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC SEQUENCE 74 BP; 3 A; 4 C; 3 G; 1 T; 63 OTHER.
SO

Query Match 3.8%; Score 25; DB 2; Length 74;
Best Local Similarity 9.9%; Pred. No. 2.03e-02;
Matches 7; Conservative 20; Mismatches 44; Indels 0; Gaps 0;

Db 3 GAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 62
Qy 432 GAGTGGCCCGCCACAGGAGTGCAGCTGCACAGGAGTGCATCACGCTGTGTGATG 491
Db 63 BNNBNACGCCA 73
Qy 492 GGTGGCGGTCA 502

RESULT 5
ID PCT-US95-11934-92 STANDARD; DNA; UNC; 81 BP.
AC xxxxxx
DE Sequence 92, Application PC/TUS9511934
CC Sequence 92, Application PC/TUS9511934
CC GENERAL INFORMATION:
CC APPLICANT: CytoGen Corporation
CC TITLE OF INVENTION: Antigen Binding Peptides (Ablides) From
CC TITLE OF INVENTION: Peptide Libraries
CC NUMBER OF SEQUENCES: 103
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Pennie & Edmonds
CC STREET: 1155 Avenue of the Americas
CC CITY: New York
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 10036
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent in Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/11934
CC FILING DATE: 20-SEP-1995
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Mistrock, S. Leslie
CC REGISTRATION NUMBER: 18,872
CC REFERENCE/DOCKET NUMBER: 1101-196-228
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212) 790-9090
CC TELEFAX: (212) 869-9741/8864
CC TELEX: 66141 PENNIE
CC INFORMATION FOR SEQ ID NO: 92:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 81 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC SEQUENCE 81 BP; 3 A; 5 C; 6 G; 4 T; 63 OTHER.
SO

Query Match 3.8%; Score 25; DB 2; Length 81;
Best Local Similarity 9.9%; Pred. No. 2.03e-02;
Matches 7; Conservative 20; Mismatches 44; Indels 0; Gaps 0;
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RESULT 11
ID PCT-US95-11934-97 STANDARD; DNA; UNC; 82 BP.
AC xxxxxx
DT Sequence 97, Application PC/TUS9511934
DE Sequence 97, Application PC/TUS9511934
CC GENERAL INFORMATION:
CC APPLICANT: Cytogen Corporation
CC TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
CC TITLE OF INVENTION: Peptide Libraries
CC NUMBER OF SEQUENCES: 103
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Pennie & Edmonds
CC STREET: 1155 Avenue of the Americas
CC CITY: New York
CC STATE: New York
CC COUNTRY: USA
CC ZIP: 10036
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/11934
CC FILING DATE: 20-SEP-1995
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Mirock, S. Leslie
CC REGISTRATION NUMBER: 18,872
CC REFERENCE/DOCKET NUMBER: 1101-196-228
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212) 790-9090
CC TELEFAX: (212) 869-9741/8864
CC TELEX: 66141 PENNIE
CC INFORMATION FOR SEQ ID NO: 97:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 82 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: DNA (genomic)
CC SEQUENCE 82 BP; 1 A; 2 C; 10 G; 8 T; 61 OTHER.
Query Match 3.7%; Score 24; DB 2; Length 82;
Best Local Similarity 10.1%; Pred. No. 6.68e-02;
Matches 7; Conservative 19; Mismatches 43; Indels 0; Gaps 0;
Db 7 CTCGAGNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNN 66
QY 43 CTCGTGGACCCGCCCTCTCTGGGGCAGCTCTACTCAGCCAT 102
Db 67 BNNBNNBG 75
QY 103 GGGGTACGG 111
RESULT 12
ID US-08-471-052A-144 STANDARD; DNA; UNC; 66 BP.
AC xxxxxx
DT Sequence 144, Application US/08471052A
DE Sequence 144, Application US/08471052A
CC Patent No. 5625033
CC GENERAL INFORMATION:
CC APPLICANT: Kay, B. K.
CC APPLICANT: Fowlkes, D. M.
CC TITLE OF INVENTION: Totally Synthetic Affinity Reagents
CC NUMBER OF SEQUENCES: 166
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Pennie & Edmonds

CC STREET: 1155 Avenue of the Americas
CC CITY: New York
CC STATE: New York
CC COUNTRY: U.S.A.
CC ZIP: 10036-2711
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/471,052A
CC FILING DATE: 06-JUNE-1995
CC CLASSIFICATION: 530
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Mirock, S. Leslie
CC REGISTRATION NUMBER: 18,872
CC REFERENCE/DOCKET NUMBER: 1101-179
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 212 790-9090
CC TELEFAX: 212 869-8864/9741
CC TELEX: 66141 PENNIE
CC INFORMATION FOR SEQ ID NO: 144:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 66 bases
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: unknown
CC MOLECULE TYPE: DNA
CC SEQUENCE 66 BP; 2 A; 3 C; 4 G; 2 T; 55 OTHER.
Query Match 3.5%; Score 23; DB 1; Length 66;
Best Local Similarity 9.7%; Pred. No. 2.15e-01;
Matches 6; Conservative 18; Mismatches 38; Indels 0; Gaps 0;
Db 4 AGNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNNBNN 63
Cp 135 AGCTCTTCCAGCAGGTAGGACCGTACCCATGCTGAGTAGAGCGTCCCCAGACA 76
Db 64 GG 65
Cp 75 GG 74
RESULT 13
ID US-08-471-052A-143 STANDARD; DNA; UNC; 68 BP.
AC xxxxxx
DT Sequence 143, Application US/08471052A
DE Sequence 143, Application US/08471052A
CC Patent No. 5625033
CC GENERAL INFORMATION:
CC APPLICANT: Kay, B. K.
CC APPLICANT: Fowlkes, D. M.
CC TITLE OF INVENTION: Totally Synthetic Affinity Reagents
CC NUMBER OF SEQUENCES: 166
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Pennie & Edmonds
CC STREET: 1155 Avenue of the Americas
CC CITY: New York
CC STATE: New York
CC COUNTRY: U.S.A.
CC ZIP: 10036-2711
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/471,052A
CC FILING DATE: 06-JUNE-1995
CC CLASSIFICATION: 530
CC ATTORNEY/AGENT INFORMATION:



Result No.	Query			ID	Description	Pred. No.
	Score	Match	Length			
C 1	498	76.4	546 15	AA724486	ah99hl1.s1 Soares NFL	0.00e+00
C 2	493	75.6	572 9	AA587126	nn70hl12.s1 NCI_CGAP_La	0.00e+00
C 3	463	71.0	567 13	AA775735	z3f104.s1 Soares feta	0.00e+00
C 4	459	70.4	563 23	AA161033	z58e04.s1 Stratagene	0.00e+00
C 5	458	70.2	610 23	AA069479	nm14hl1.s1 Stratagene	0.00e+00
C 6	452	69.3	568 10	AA595715	n146e08.s1 NCI_CGAP_Lu	0.00e+00
C 7	446	68.4	591 11	AA643068	zr95f04.s1 NCI_CGAP_Pr	0.00e+00
C 8	442	67.8	556 8	AA210894	zr90g06.s1 NCI_CGAP_GC	0.00e+00
C 9	437	67.0	541 11	AA479680	zu43a07.s1 Soares ovar	0.00e+00
C 10	435	65.2	541 15	AA748434	ny01b10.s1 NCI_CGAP_GC	0.00e+00
C 11	424	65.0	506 7	AA456315	aal13g10.s1 Soares NhhM	0.00e+00
C 12	414	63.5	551 5	AA036726	zk30b07.s1 Soares preg	0.00e+00
C 13	405	62.1	505 16	AA838533	oe39a11.s1 NCI_CGAP_Pr	0.00e+00

I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."
/db_xref="taxon:9606"
/clone="1327269"
/clone_lib="Soares NFL T GBC SI"
/lab_host="DH10B"
/lab="166 c 166 g 91 t 3 others

BASE COUNT 120 a 166 c 166 g 91 t 3 others
ORIGIN
Query Match 76.4%; Score 498; DB 15; Length 546;
Best Local Similarity 98.4%; Pred. No. 0.00e+00;
Matches 503; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Db 36 AAATTCATGTTCCAGAACATGCTTAAGCATGCGAGAAAGCAGACGACACTGCTCCCGG 95
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Cp 652 AAATTCATGTTCCAGAACATGCTTAAGCATGCGAGAAAGCAGACGACACTGCTCCCGG 593
Db 96 GTGGGGCTCAGTGGGGCCACCTCTGAAGCTCTGCTGACCCCTGGGCGAAGGCGCTGAC 155
|||||
Cp 592 GTGGGGCTCAGTGGGGCCACCTCTGAAGCTCTGCTGACCCCTGGGCGAAGGCGCTGAC 533
Db 156 AGACTAGCAGGCGCCAGTGGTGTATGAAGCGTGACGGCCACCATCACAAGCGTGATGCG 215
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Cp 532 AGACTAGCAGGCGCCAGTGGTGTATGAAGCGTGACGGCCACCATCACAAGCGTGATGCG 473
Db 216 ACCTGCTGTGCTCANGCTGCGCTCCCTGTGGGGCGGGCGGCGCTCCTGCGAGCGCGCTCC 275
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Cp 472 ACCTGCTGTGCTCANGCTGCGCTCCCTGTGGGGCGGGCGGCGCTCCTGCGAGCGCGCTCC 413
Db 276 CCCAGCCAGCCATGGTGTGCCGCCATACGCGAGTAGTTGAGTGTGCTGTAAGGCGCAG 335
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Cp 412 CCCAGCCAGCCATGGTGTGCCGCCATACGCGAGTAGTTGAGTGTGCTGTAAGGCGCAG 353
Db 336 CCAGCGCAGGTAGGCGTAGAGAGCGGGCGGCGGCGGCGCTCCTGCTACCGAGCGCCAC 395
Cp 352 CCAGCGCAGGTAGGCGTAGAGAGCGGGCGGCGGCGGCGCTCCTGCTACCGAGCGCCAC 293
Db 396 GGTAGTGTGNCNGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 455
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Cp 292 GGTAGTGTGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 233
Db 456 TCGGGCACAAGAAGATGGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 515
Cp 232 TCGGGCACAAGAAGATGGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 173
Db 516 GCCCAGGGGAACACAGCGCTCTCTGTGAAG 546
Cp 172 GCCCAGGGGAACACAGCGCTCTCTGTGAAG 142

RESULT 2 AA587126 572 bp mRNA EST 12-SEP-1997
LOCUS nn70b12.s1 NCI_CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1089215
DEFINITION similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR
(HUMAN); mRNA sequence.
ACCESSION AA587126
NID 92397940
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 572)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.

Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Seq primer: -40ml3 fwd. Et from Amersham
High quality sequence stop: 462.

FEATURES
source

Location/Qualifiers
1..572

/organism="Homo sapiens"
/note="Organ: larynx; Vector: Bluescript SK-; Site_1:
ECORI; Site_2: XhoI; cloned unidirectionally. Primer:
Oligo dt. Larynx. 5' adaptor sequence: 5' GAATTCGCGCAGG
3' 3' adaptor sequence: 5' CnCGAGTTTTTTTTTTTTTTT 3'
Average insert size: 0.9 kb."
/db_xref="taxon:9606"
/clone="IMAGE:1089215"
/clone_lib="NCI_CGAP_Lar1"
/tissue_type="larynx"
/lab_host="SOLR (kanamycin resistant)"
<1..>572

mRNA 132 a 171 c 173 g 96 t
BASE COUNT
ORIGIN

Query Match 75.6%; Score 493; DB 9; Length 572;
Best Local Similarity 96.5%; Pred. No. 0.00e+00;
Matches 522; Conservative 0; Mismatches 17; Indels 2; Gaps 2;

Db 34 AAATTCATGTTCCAGAACATGCTTAAGCATGCGAGAAAGCAGACGACACTGCTCCCGG 93
Cp 652 AAATTCATGTTCCAGAACATGCTTAAGCATGCGAGAAAGCAGACGACACTGCTCCCGG 593
Db 94 GTGGGGCTCAGTGGGGCAACCTCTGAAGCTCTGCTGACCCCTGGGCGCAGGCGCTGAC 153
Cp 592 GTGGGGCTCAGTGGGGCAACCTCTGAAGCTCTGCTGACCCCTGGGCGCAGGCGCTGAC 533
Db 154 AGACTAGCAGGCGCGAGTGGTGTATGAAGCGTGAGCGGCGGCGGCGGCGGCGGCGGCGG 213
Cp 532 AGACTAGCAGGCGCGAGTGGTGTATGAAGCGTGAGCGGCGGCGGCGGCGGCGGCGGCGG 473
Db 214 ACCTGCTGTGCGAGCTGCGTCCCTGGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 273
Cp 472 ACCTGCTGTGCGAGCTGCGTCCCTGGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 413
Db 274 CCATGCCAGCCATGGTGTCCGCCATAGCGAGTAGTTGAGTGTGCTGCGGAAGGCGCAG 333
Cp 412 CCCACGCCAGCCATGGTGTCCGCCATAGCGAGTAGTTGAGTGTGCTGGAAGGCGCAG 353
Db 334 CCAGGCGCAGGTAGGGGTAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 393
Cp 352 CCAGGCGCAGGTAGGGGTAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 293
Db 394 GGTAGTGTGACCGG 453
Cp 292 GGTAGTGTGCGG 233
Db 454 TCGGGCACAAGAAGATGGGGAGGCCATGCCAGTTCCAGGGCGCAGCTGCGACAGGTGTAGAG 513
Cp 232 TCGGGCACAAGAAGATGGGGAGGCCATGCCAGTTCCAGGGCGCAGCTGCGCGCGCGCGCGG 173
Db 514 GCCCAGGGGAAC-ACAGCCTTCTGTGGAAGACTCCCGAGCTCTTTC-AGACCGAGGTATGA 571
Cp 172 GCCCAGGGGAACACAGCGCTTCTGTGGAAGCGCTCCCGAGCTCTTTCACGAGCGGTAGGA 113
Db 572 G 572
Cp 112 G 112
RESULT 3

LOCUS AA775735 567 bp mRNA EST 05-FEB-1998
DEFINITION zf3if04.s1 Soares fetal heart NBHH19W Homo sapiens cDNA clone
378559 3' similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE
RECEPTOR (HUMAN)). mRNA sequence.
ACCESSION AA775735
NID 92835059
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 567)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krisman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marras,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wylie,T., Waterston,R. and Willson,R.
TITLE WashU-NCI human EST project
JOURNAL Unpublished (1997)
COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: ~40m13 fwd. ET from Amersham
High quality sequence stop: 487.
FEATURES
Location/Qualifiers
1..567
/organism="Homo sapiens"
/note="organ: heart; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCACTGAGTGGAGCGCGCATCTTTTCTTTTCTTTT 3']
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M.Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NBHL19W."
/db_xref="GDB:1286815"
/db_xref="taxon:9606"
/clone="378559"
/clone_lib="Soares fetal heart NBHH19W"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
167 c 175 g 98 t 1 others
BASE COUNT 126 a
ORIGIN

Query Match 71.0%; Score 463; DB 13; Length 567;
Best Local Similarity 96.3%; Pred. No. 0.00e+00;
Matches 522; Conservative 0; Mismatches 12; Indels 8; Gaps 8;

Db 30 AAATTCATGTTCCAGACATGCTCTAAGCATGAGAAAGCAGACACTGCTCCCGG 89
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Cp 652 AAATTCATGTTCCAGACATGCTCTAAGCATGAGAAAGCAGACACTGCTCCCGG 593
|||||
Db 90 GTGGGGGCTCAGTGGGGCCACTCTGTAAGCTCTGCTGACCCCTGGCGCAAGGCGCTGAC 149
|||||
Cp 592 GTGGGGGCTCAGTGGGGCCACTCTGTAAGCTCTGCTGACCCCTGGCGCAAGGCGCTGAC 533
|||||
Db 150 AGACTAGCAGGGCCCACTGGTGCATGAAGCGTGACGGGCCACCACATCATCAAGCGTGATGGC 209
|||||
Cp 532 AGACTAGCAGGGCCCACTGGTGCATGAAGCGTGACGGGCCACCACATCATCAAGCGTGATGGC 473
|||||
Db 210 ACCTGCTGTGTG-AGCTGCACTCCCTGTGTGGCGCGGCGCACTCACTCTGGCAGCGCGCGTCC 268
|||||
Cp 472 ACCTGCTGTGTGAGCTGCACTCCCTGTGTGGCGCGGCACTCACTCTGGCAGCGCGCGTCC 413
|||||

Query Match 70.4%; Score 459; DB 23; Length 563;
Best Local Similarity 96.2%; Pred. No. 0.00e+00;
Matches 533; Conservative 0; Mismatches 13; Indels 7; Gaps 7;

Db 35 AAATTCATGTTCCAGAACATGCTCTAAGCATGCAGAAAGCAGAGACATGCTCCCGG 94
Cp 652 AAATTCATGTTCCAGAACATGCTCTAAGCATGCAGAAAGCAGAGACATGCTCCCGG 593

Db 95 GTGGGGCTCAGGTGGGCGACCTCTGAAGCTCTGCTACCCCTGGGCGAAGGCCATGAC 154
Cp 592 GTGGGGCTCAGGTGGGCGACCTCTGAAGCTCTGCTACCCCTGGGCGAAGGCCCTGAC 533

Db 155 AGACTAGCAGCCAGTGGTGCATGAAGCGTGAGCGGCCACACATCACAAGCGTGATGGC 214
Cp 532 AGACTAGCAGCCAGTGGTGCATGAAGCGTGAGCGGCCACACATCACAAGCGTGATGGC 473

Db 215 ACCTGCTGGTN-AGCTGCAGTCCCTGTGGCGGGCAGTCTGCTGACGCCCGCTCC 273
Cp 472 ACCTGCTGGTGCAGTGCAGTCCCTGTGGCGGGCAGTCTGCTGACGCCCGCTCC 413

Db 274 CCCATGCCAGCATGGTGTCCCGCCATACGCAGTAGTTGAGTGTGGTGGCGAAGGCCAG 333
Cp 412 CCCAGCGCAGCATGGTGTCCCGCCATACGCAGTAGTTGAGTGTGGTGGCGAAGGCCAG 353

Db 334 CCAGCCAGGTAAAGGGGTAGAGCAGCGGGCGGCGAGCGGGCTTCACTGGTACCAGGC 393
Cp 352 CCAGCCAGGTA-GGGTAGAGCAGCGGGCGGCGAGCGGG-CT-CACCTGGTACCAGGC 296

Db 394 CACGGTAGTTGGC-CCGCGCGCCCTCACTGACGAGGAGATCCACCAAGGCCCGCCCAT 452
Cp 295 CACGGTAGTTGGTGGCGCGCCCTCACTGACGAGGAGATCCACCAAGGCCCGCCCAT 236

Db 453 TTGTCGGCACCAAGAGATGGGGGCGCATGCAAGTTTCAGGGCCAGCTGCC-AGTGTA 511
Cp 235 TTGTCGGCACCAAGAGATGGGGGCGCATGCCAGTTTCAGGGCCAGCTGCCAGTGTGA 176

Db 512 GAGGCCAGGGGAACACAGAGCTTCTGTGAAGCTTCC-AGCTCTTTCCAGA 563
Cp 175 GAGGCCAGGGGAACACAGAGCTTCTGTGAAGCTTCCAGCTTCCAGCTTTCCAGA 123

RESULT 5
LOCUS AA069479 610 bp mRNA EST 23-DEC-1997
DEFINITION zml4h11.s1 Stracagene pancreas (#937208) Homo sapiens cDNA clone 525669 3', similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (HUMAN);, mRNA sequence.

ACCESSION AA069479
NID g1577104
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 610)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.
Washu-Werck EST Project
Unpublished (1995)

TITLE Contact: Wilson RK
JOURNAL Washington University School of Medicine
COMMENT 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
WARNING: There is evidence that suggests that the 384-well parent plate of this clone contains both human and mouse derived clones. Thus, the origin of this clone is uncertain. This caution should be kept in mind should you use this clone.

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 951 Std Error: 0.00
Seq primer: -40M13 fwd. from Amersham
High quality sequence stop: 118.

FEATURES
source 1..610
Location/Qualifiers
/organism="Homo sapiens"
/note="Organ: pancreas; Vector: pBluescript SK-; Site: 1: EcoRI; Site: 2: XhoI; Cloned unidirectionally. Primer: Oligo dr. Pancreatic adenocarcinoma cell line. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGACGAG 3' -3' adaptor sequence: 5' CTCGAGTCTTTTCTTTTCTTTT 3'";
/db_xref="GDB:3917098"
/db_xref="taxon:9606"
/clone="525669"
/clone_lib="Stracagene pancreas (#937208)"
/lab_host="SOLR cells (kanamycin resistant)"

BASE COUNT 133 a 177 c 175 g 103 t 22 others
ORIGIN

Query Match 70.2%; Score 458; DB 12; Length 610;
Best Local Similarity 92.3%; Pred. No. 0.00e+00;
Matches 527; Conservative 0; Mismatches 35; Indels 9; Gaps 8;

Db 33 AAATTCATGTTCCAGAACATGCTCTAAGCATGCAGAAAGCAGAGACATGCTCCCGG 92
Cp 652 AAATTCATGTTCCAGAACATGCTCTAAGCATGCAGAAAGCAGAGACATGCTCCCGG 593

Db 93 GTGGGGCTCAGGTGGGCGCACCTCTGAAGCTCTGCTGACCCCTGGGCGCAAGGCC-TGAC 151
Cp 592 GTGGGGCTCAGGTGGGCGCACCTCTGAAGCTCTGCTGACCCCTGGGCGCAAGGCCGTGAC 533

Db 152 AGACTAGCAGCCAGTGGTGCATGAAGCGTGAGCGGCCACACATCACAAGCGTGATGGC 211
Cp 532 AGACTAGCAGCCAGTGGTGCATGAAGCGTGAGCGGCCACACATCACAAGCGTGATGGC 473

Db 212 ACCTGCTGGT-CAGCTCAGTCCCTGGTGGCGGGCGACCTCTGTCGAGNCGCCGCTCC 270
Cp 472 ACCTGCTGGTGCAGTGCAGTCCCTGGTGGCGGGCGACCTCTGTCGAGCGCCGCTCC 413

Db 271 CCCAGCGCAGCCATNGTGTCCCGCCNTACTCAGTAGTTGAGTNGTGTGCGAAGGCCAG 330
Cp 412 CCCAGCGCAGCCATNGTGTCCCGCCNTACTCAGTAGTTGAGTNGTGTGCGAAGGCCAG 353

Db 331 CCAGCCAGTATGGGTAGAGCAGCGGGCGGCCGCTACCTGCTACCAAGGCCAC 390
Cp 352 CCAGCCAGTATGGGTAGAGCAGCGGGCGGCCGCTACCTGCTACCAAGGCCAC 293

Db 391 GGTATTTGC--CCGCGCGCCCTNACGAGNAGNAGGATTCCACCAAGGCCAGCCCATTT 448
Cp 292 GGTAGTGGTGGCGCGCCCTNACGAGNAGNAGGATTCCACCAAGGCCAGCCCATTT 234

Db 449 GTCGGGACCAAGAAAGATNGGGGGCATGCC-AGTTTCAGGGC-AGNTGCCNAGTGTAGA 506
Cp 233 GTCGGGACCAAGAAAGATNGGGGGCATGCCCAAGTTTCAGGGCGAGCTGCCAGTGTAGA 174

Db 507 GGCCCGAGTGAACACACANGCTTCTCTGTGNAGC-TCCAG-TNNTTCCAGACCAAGTNGG 564
Cp 173 GGCCCGAGTGAACACACANGCTTCTCTGTGAAGCTTCCAGCTCTTCCAGACCAAGTAGG 114

Db 565 AGCGCTNNCCATGGCTANGTAGAGCTTCCG 595
Cp 113 AGCGCTACCCCATGGCTGAGTAGAGCGTGGC 83

RESULT 6
LOCUS AA595715 568 bp mRNA EST 25-SEP-1997
DEFINITION n146e08.s1 NCI-CGAP_Lu1 Homo sapiens cDNA clone IMAGE:979910 similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (HUMAN);, mRNA sequence.
ACCESSION AA595715

NID 92411065
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 568)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 JOURNAL
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert_Strausberg@nih.gov
 Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: Stratagene, Inc., David B. Krizman,
 Ph.D.
 CDNA Library Arraying: Greg Lennon, Ph.D.
 DNA sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 713 Std Error: 0.00
 Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 265.
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 Location/Qualifiers
 1..568
 /organism="Homo sapiens"
 /note="Organ: lung; Vector: Bluescript SK-; Site_1: EcoRI;
 Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT.
 Bulk lung tumor. 5' adaptor sequence: 5' GAATTCGGCAGCAG 3'
 3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'
 Average insert size: 1.1 kb."
 /db_xref="taxon:9606"
 /clone="IMAGE:979910"
 /clone_lib="NCI_CGAP_Lul"
 /tissue_type="lung tumor"
 /lab_host="SOLR (kanamycin resistant)"
 BASE COUNT 124 a 164 c 165 g 113 t 2 others
 ORIGIN
 Query Match 69.3%; Score 452; DB 10; Length 568;
 Best Local Similarity 96.9%; Pred. No. 0.00e+00;
 Matches 496; Conservative 0; Mismatches 10; Indels 6; Gaps 6;
 Db 53 AAATTCCATGTTCCAGAACATGCTCTAAGCATGCAGAAACAGACAGACTGCTCCCGG 112
 Cp 652 AAATTCCATGTTCCAGAACATGCTCTAAGCATGCAGAAACAGACAGACTGCTCCCGG 593
 Db 113 GTGGGGCTCAGGTGGGGCCACCTCTGAGCTCTGCTGACCCCTGGGCCAGGCCCTGAC 172
 Cp 592 GTGGGGCTCAGGTGGGGCCACCTCTGAGCTCTGCTGACCCCTGGGGCAGAGCCCTGAC 533
 Db 173 AGACTAGCAGGCCAGTGGTGCATGAAGCGTGACGGCCACACATCAACAGCGTGATGGC 232
 Cp 532 AGACTAGCAGGCCAGTGGTGCATGAAGCGTGACGGCCACACATCAACAGCGTGATGGC 473
 Db 233 ACCTGCTGGTGTAGCTGAGTCCCTGTGGGCCGGGCACTCACTCTGGCAGCCCGCTCC 292
 Cp 472 ACCTGCTGGTGTAGCTGAGTCCCTGTGGGCCGGGCACTCACTCTGGCAGCCCGCTCC 413
 Db 293 CCCAGCCAGCCATGGTGTCTCCGCCATACGCAGTAGTTGAGTGTGCTGTGAAGGCCAG 352
 Cp 412 CCCAGCCAGCCATGGTGTCTCCGCCATACGCAGTAGTTGAGTGTGCTGTGAAGGCCAG 353
 Db 353 CCAGCCAGGTAGGGGTAGACGCGGGCCGCGGCTCACCTGGTACCAGGCCAC 412
 Cp 352 CCAGCCAGGTAGGGGTAGACGCGGGCCGCGGCTCACCTGGTACCAGGCCAC 293
 Db 413 GGTACTGGNN-CCGCGCGCCCACTGACACGACGAGGAGATCCACCAGGCCACCCATTG 471

Cp 292 GGTAGTGGTGGCGCGCCCACTGACCAGCAGGAGATCCACCAAGGCCAGCCCATTTG 233
 Db 472 TCGGGCACCACAAAGATGGGGCCCATGCAC-GTCTAGGCGAGCTGCCAA-TGTAGAG 529
 Cp 232 TCGGGCACCACAAAGATGGGGCCCATGCCAGTTTCAGGCCAGCTGCCCATGTAGAG 173
 Db 530 GCCAAGGG-AAC-ACAGC-TTCTCTGTGAAGC 558
 Cp 172 GCCCAGGGGAACACACAGCCTTCTCTGTGAAGC 141
 RESULT 7
 LOCUS AA643068 591 bp mRNA EST 27-OCT-1997
 DEFINITION nr95f04.s1 NCI_CGAP_Pr25 Homo sapiens cDNA clone IMAGE:1175743
 similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR
 (HUMAN); mRNA sequence.
 ACCESSION AA643068
 NID 92568286
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 591)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 JOURNAL
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert_Strausberg@nih.gov
 Tissue Procurement: Suzanne L. Topalian, M.D., Robert K. Bright,
 Ph.D.
 CDNA Library Preparation: Stratagene, Inc.
 DNA sequencing by: Greg Lennon, Ph.D.
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 337.
 FEATURES
 source
 Location/Qualifiers
 1..591
 /organism="Homo sapiens"
 /note="Organ: prostate; Vector: Bluescript SK-; Site_1:
 EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
 Oligo dT. Normal prostate epithelial cell line (HPV
 immortalized). 5' adaptor sequence: 5' GAATTCGGCAGCAG 3'
 3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'
 Average insert size: 1.1 kb."
 /db_xref="taxon:9606"
 /clone="IMAGE:1175743"
 /clone_lib="NCI_CGAP_Pr25"
 /tissue_type="epithelium (cell line)"
 /lab_host="SOLR (kanamycin resistant)"
 BASE COUNT 131 a 179 c 181 g 97 t 3 others
 ORIGIN
 Query Match 68.4%; Score 446; DB 11; Length 591;
 Best Local Similarity 95.4%; Pred. No. 0.00e+00;
 Matches 544; Conservative 0; Mismatches 11; Indels 15; Gaps 15;
 Db 28 AAATTCCATGTTCCAGAACATGCTCTAAGCATGCAGAAACAGACAGACTGCTCCCGG 87
 Cp 652 AAATTCCATGTTCCAGAACATGCTCTAAGCATGCAGAAACAGACAGACTGCTCCCGG 593
 Db 88 GTGGGGCTCAGGTGGGGCCACCTCTGAAGCTGTGCTGACCCCTGGGCCAAGGCCCTGAC 147
 Cp 592 GTGGGGCTCAGGTGGGGCCACCTCTGAAGCTGTGCTGACCCCTGGGCCAAGGCCCTGAC 593

148 AGACTAGCAGGCCAGTGGTTCATGAAGCGTGACGGCCACACATCACAAGCGTGATGGC 207
|||||
532 AGACTAGCAGGCCAGTGGTTCATGAAGCGTGACGGCCACACATCACAAGCGTGATGGC 473
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208 ACCTGCTGGTG-AGCTGAGTCCCTGTGTGGCGGGGCACTCTCTGGCAGCGCC-GTCC 265
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472 ACCTGCTGGTGAGTCCCTGTGTGGCGGGGCACTCTCTGGCAGCGCCGTCC 413
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266 CCCAGCGCCAGCGTGTGTCCCGCCATAGCAGTGTGAGTGTGCTGCGAAGGCCAG 325
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412 CCCAGCGCCAGCGTGTGTCCCGCCATAGCAGTGTGAGTGTGCTGGAAGGCCAG 353
|||||
326 CCAGCGCAGGTAGGGTAGAGCAGCGCGCGCGGCGGCTCACCTGGTACAGGCCAC 385
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352 CCAGCGCAGGTAGGGTAGAGCAGCGCGCGCGGCGGCTCACCTGGTACAGGCCAC 293
|||||
386 GGTACTGGNMC-CCGCGCCCACTGACAGCAGGAGATCCACCAAGGCCAGGCCATTG 444
|||||
292 GGTAGTGGTCTGCCCGCCCACTGACAGCAGGAGATCCACCAAGGCCAGGCCATTG 233
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445 TCGGGCAC-AAAGAGATGGGGGCCATGCC-AGTTCAGGCGCCAGCTGCC-AGTGTAGAN 501
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232 TCGGGCACAAAGAGATGGGGGCCATGCCAGTTCAGGCGCCAGCTGCCAGTGTAGAG 173
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502 GCC-AGGGGAAC-ACAGC-TTCTCTGTGAAGCCCTCC-AGCTCTTTTC-AGAC-AGGTAGGA 555
|||||
172 GCCCAGGGGAACACAGCCTTCTCTGTGAAGCCCTCCAGCTCTTTCCAGACCCAGGTAGGA 113
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556 GC-GTACCC-ATG-CTGAGTGTAGCTGTGCC 582
|||||
112 GCCGTACCCCATGGCTGAGTAGCGGTGCC 83
|||||

RESULT 8
LOCUS AA210894 556 bp mRNA EST 13-AUG-1997
DEFINITION zf90g06.s1 NCI-CGAP_GCB1 Homo sapiens cDNA clone IMAGE:683002 3' similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (HUMAN);, mRNA sequence.
ACCESSION AA210894
NID g1809540
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 556)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 428.
Location/Qualifiers
1. .556
/organism="Homo sapiens"
/note="Vector: p7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+ IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAAGTGGGCGCGCTCATTTTTTTTTTTTTTT-3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7T3 vector. Library

went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."
/db_xref="taxon:9606"
/clone="IMAGE:683002"
/clone_lib="NCI-CGAP_GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
complement(<1..>556)
/db_xref="GDB:5586322"
BASE COUNT 122 a 160 c 164 g 104 t 6 others
ORIGIN

Query Match 67.8%; Score 442; DB 8; Length 556;
Best Local Similarity 96.9%; Pred. No. 0.00e+00;
Matches 473; Conservative 0; Mismatches 11; Indels 4; Gaps 4;

Db 43 AAATTCATGTTCCAGAACAATGCTCTAAGCATGCGAGAAGACACAGACACTGCTCCCG 102
|||||
Cp 652 AAATTCATGTTCCAGAACAATGCTCTAAGCATGCGAGAAGACACAGACACTGCTCCCG 593
|||||
Db 103 GTGGGGCTCAGTGGGGCCACCTCTGAAGCTCTGTGACCCCTGGGCGCAAGGCCNTGAC 162
|||||
Cp 592 GTGGGGCTCAGTGGGGCCACCTCTGAAGCTCTGTGACCCCTGGGCGCAAGGCCNTGAC 533
|||||
Db 163 AGACTAGCAGGCCAGTGTGATGAAGCGTGACGCCACACATCACAAGCGTGTATGGC 222
|||||
Cp 532 AGACTAGCAGGCCAGTGTGATGAAGCGTGACGCCACACATCACAAGCGTGTATGGC 473
|||||
Db 223 ACCTGCTGTGTT-AGCTGCGAGTCCCTGTGGCGGGCGCACTCACTCTGGCAGCGCGCTCC 281
|||||
Cp 472 ACCTGCTGTGAGCTGCGAGTCCCTGTGGCGGGCGCACTCACTCTGGCAGCGCGCTCC 413
|||||
Db 282 CCCACGCCAGCCATGGTTGTCCCGCCATAGCAGTAGTGTGAGTGTGTCGCGAAGGCCAG 341
|||||
Cp 412 CCCACGCCAGCCATGGTTGTCCCGCCATAGCAGTAGTGTGAGTGTGTCGCGAAGGCCAG 353
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Db 342 CCAGGCCAGTGTAGGTTAGAGAGGGGGGGCGGCGGCTACCTGTGTACAGGCCAC 401
|||||
Cp 352 CCAGGCCAGTGTAGGTTAGAGAGGGGGGGCGGCGGCTACCTGTGTACAGGCCAC 293
|||||
Db 402 GGTAGTTTNCNCCGCGCCGCTGACAGCAGGAGATTACCAAGGCCAGGCCATTG 461
|||||
Cp 292 GGTAGTGTGCGCGCGCGCCCTGACAGCAGGAGATCCACCAAGGCCAGGCCATTG 233
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Db 462 TCGGGCACCAAAAGATGGGGGCG-ATGCC-AGTTTCAGGCCAGCTGCC-AGTGTANAG 518
|||||
Cp 232 TCGGGCACCAAAAGATGGGGGCGCATGCCAGTTTCAGGCCAGCTGCCAGCTGTAGAG 173
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Db 519 GCCAAGGG 526
|||||
Cp 172 GCCCAGGG 165
|||||

RESULT 9
LOCUS AA479680 541 bp mRNA EST 09-NOV-1997
DEFINITION zu43a07.s1 Soares ovary tumor Nshot Homo sapiens cDNA clone 740724 3' similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (HUMAN);, mRNA sequence.
ACCESSION AA479680
NID Q2205566
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 541)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Scheinberg, K., Steptoe, M., Tan, F., Thaising, B., White, Y., Wyllie, T., Waterston, R. and Wilson, R.
TITLE WashU-NCI human EST Project
JOURNAL Unpublished (1997)
COMMENT

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewartson.wustl.edu

This clone is available royalty-free through LLNL : contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 598 Std Error: 0.00
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 52.

FEATURES

source
1..541
/organism="Homo sapiens"
/note="Organ: ovary; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTCAAGTGGGAGCGCGGTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library constructed by Bento Soares and
M. Fatima Bonaldo."
/db_xref="GDB:5940628"
/db_xref="taxon:9606"
/clone_lib="Soares ovary tumor NBHOT"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
BASE COUNT 111 a 155 c 159 t 1 others
ORIGIN

Query Match 67.0%; Score 437; DB 11; Length 541;
Best Local Similarity 97.9%; Pred. No. 0.00e+00;
Matches 461; Conservative 0; Mismatches 7; Indels 3; Gaps 3;
Db 73 AAATTCCATGTTCCAGAACATGCTCTAAGCATGCAGAAAGCAGGACACTGCTCCCGG 132
|||||
Cp 652 AAATTCCATGTTCCAGAACATGCTCTAAGCATGCAGAAAGCAGGACACTGCTCCCGG 593
|||||
Db 133 GTGGGGCTCAGGTGGGCGCCACCTCTGAAGCTCTGCTGACCCCTGGCGGAGGCTCGAC 192
|||||
Cp 592 GTGGGGCTCAGGTGGGCGCCACCTCTGAAGCTCTGCTGACCCCTGGCGGAGGCTCGAC 533
|||||
Db 193 AGACTAGCAGGCCCGGAGTGGTTCATGAAGCGTGAAGCGGCGCCACCATCATCAAGCGTGAATGGC 252
|||||
Cp 532 AGACTAGCAGGCCCGGAGTGGTTCATGAAGCGTGAAGCGGCGCCACCATCATCAAGCGTGAATGGC 473
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Db 253 ACCTGCTGGTGAAGCTGACGTCCTGTGGGCGGCGGCACTCACTCTGGCAGCCCGCTCC 312
|||||
Cp 472 ACCTGCTGGTGAAGCTGACGTCCTGTGGGCGGCGGCACTCACTCTGGCAGCCCGCTCC 413
|||||
Db 313 CCCAGCGCAGCCATGTTGTCCTCCGCCATACCGACTAGTGTGAGTGTGTCGCGAAGGCCAG 372
|||||
Cp 412 CCCAGCGCAGCCATGTTGTCCTCCGCCATACCGACTAGTGTGAGTGTGTCGCGAAGGCCAG 353
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Db 373 CCAGCGCAGGTAGGGTAGACAGCGGGCGGCCAGCGGGCTCCACCTGTGACCAAGGCCA 432
|||||
Cp 352 CCAGCGCAGGTAGGGTAGACAGCGGGCGGCCAGCGGGCTC-ACCTGTGACCAAGGCCA 294
|||||
Db 433 CGGTAGTGGCNGC-GCCGCCCCACTGACACAGGAGATGCCAACCAAGGCCCGCCCAATTT 491
|||||
Cp 293 CGGTAGTGGTGGCCTGCCCGCCCACTGACACAGGAGATGCCAACCAAGGCCCGCCCAATTT 234
|||||
Db 492 GTCGGGCACCAAGAGATGGGGGCCATGCC-AGTTCAGGGCCAGCTGCC 541
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Cp 233 GTCGGGCACCAAGAGATGGGGGCCATGCCAGTTCAGGGCCAGCTGCC 183
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RESULT 10
LOCUS AA748434 541 bp mRNA EST 18-FEB-1998
DEFINITION ny01b10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1270459

similar to gb:U12421.cds1 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR
(HUMAN);, mRNA sequence.

ACCESSION
AA748434

NID
92788392

KEYWORDS
EST.

SOURCE
human.

ORGANISM
Homo sapiens

REFERENCE
1 (bases 1 to 541)

AUTHORS
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Location/Qualifiers

1..541

Unpublished (1997)

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,

Ph.D., Gerald Marti, M.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 874 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 358.

Location/Qualifiers

1..541

/organism="Homo sapiens"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified

polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA

was prepared from human tonsillar cells enriched for

germinal center B cells by flow sorting (CD20+, IgD-),

provided by Dr. Louis M. Staudt (NCI), Dr. David Allman

(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was

primed with a Not I - oligo(dT) primer

[5'-TGTTACCAATCTCAAGTGGGAGCGCGCTCATTTTTTTTTTTTTT-

3']. Double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT7T3 vector. Library

went through one round of normalization, and was

constructed by Bento Soares and M. Fatima Bonaldo."

/db_xref="taxon:9606"

/clone_lib="IMAGE:1270459"

/clone_lib="NCI_CGAP_GCB1"

/tissue_type="germinal center B cell"

/lab_host="DH10B"

BASE COUNT 120 a 152 c 166 g 100 t 3 others

ORIGIN

Query Match 65.2%; Score 425; DB 15; Length 541;

Best Local Similarity 94.7%; Pred. No. 0.00e+00;

Matches 463; Conservative 0; Mismatches 23; Indels 3; Gaps 3;

Db 50 AAATTCCATGTTCCAGAACATGCTCTAAGCATGCAGAAAGCAGGACACTGCTCCCGG 109

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Cp 652 AAATTCCATGTTCCAGAACATGCTCTAAGCATGCAGAAAGCAGGACACTGCTCCCGG 593

|||||

Db 110 GTGGGGCTCAGGTGGGCGCCACCTCTGAAGCTCTGCTGACCCCTGGCGGAGGCTCGAC 169

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Cp 592 GTGGGGCTCAGGTGGGCGCCACCTCTGAAGCTCTGCTGACCCCTGGCGGAGGCTCGAC 533

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Db 170 AGACTAGCAGGCCCGGAGTGGTTCATGAAGCGTGAAGCGGCGCCACCATCATCAAGCGTGAATGGC 229

|||||

Cp 532 AGACTAGCAGGCCCGGAGTGGTTCATGAAGCGTGAAGCGGCGCCACCATCATCAAGCGTGAATGGC 473

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Db 230 ACCTGCTGGTGAAGCTGACGTCCTGTGGGCGGCGGCACTCACTCTGGCAGCGGC-GTCC 288

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Cp 472 ACCTGCTGGTGCAGTGCAGTCCCTGGTGGGCGGCGCACTCACTTGGCAGCGCCGCTCC 413
Db 289 CCCAGCCAGCCATGTTGTTCCCGCATACGACGAGTAGTGTGGTGGCGAAGGCCAG 348
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Cp 412 CCCAGCCAGCCATGTTGTTCCCGCATACGACGAGTAGTGTGGTGGCGAAGGCCAG 353
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Cp 352 CCAGGCCAGGTAGGGGTAGAGCAGCGGGCGGCCAGCGGGT-CACCTGGTAGAGGCCA 294
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Db 409 CGGTAGGTGNNCGGCCCGCCCACTGACGACGAGAGATTACCAAGGCCCGCCGCAATTT 468
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Cp 293 CGGTAGGTGCTCCCGCCCGCCCACTGACGACGAGAGATCCACCAAGGCCCGCCGCAATTT 234
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Cp 233 GTCCGGCCACCAAGATAGTGGGGGCGCATGCCAGTTCAGGGCCAGCTGCCAGTGTAGA 174
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Db 528 GGGCCAGGG 536
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Cp 173 GGCCAGGG 165

RESULT 11
LOCUS AA456315 506 bp mRNA EST 06-JUN-1997
DEFINITION aa13910.s1 Soares NHMPu S1 Homo sapiens cDNA clone 813186 3',
similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR
(HUMAN);, mRNA sequence.
ACCESSION AA456315
NID 92179525
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Euthera; Primates; Catarrhini; Hominiidae;
Homo.
REFERENCE 1 (bases 1 to 506)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le.N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
JOURNAL Unpublished (1997)
TITLE
JOURNAL
COMMENT
Contact: wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 443.
FEATURES
Location/Qualifiers
source
1..506
/organism="Homo sapiens"
/note="Organ: mixed (see below); Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site.1: Not I;
Site.2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NBHM, pregnant uterus
NbHPU, and fetal heart NbHH19) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
/db_xref="taxon:9606"
/clone="813186"
/clone_lib="Soares NHMPu S1"
/tissue_type="Pooled human melanocyte, fetal heart, and

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pregnant uterus"
/lab_host="DH10B"
complement(<1..>506)
/db_xref="GDB:6044096"
BASE COUNT 114 a 130 c 158 g 83 t 1 others
ORIGIN
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Best Local Similarity 96.9%; Pred. No. 0.00e+00;
Matches 463; Conservative 0; Mismatches 10; Indels 5; Gaps 5;
Db 34 AAATTCATGTTTCCAGAACATGCTCTAAGCATGCGAGAAAGACAGGACACTGCTCCCGG 93
Cp 652 AAATTCATGTTTCCAGAACATGCTCTAAGCATGCGAGAAAGACAGGACACTGCTCCCGG 593
Db 94 GTGGGGCTCAGTGGGGCAACCTCTGAAGCTCTGTGACCCCTGGGCCAAGGCCCTGAC 153
Cp 592 GTGGGGCTCAGTGGGGCAACCTCTGAAGCTCTGTGACCCCTGGGCCAAGGCCCTGAC 533
Db 154 AGACTAGCAGGCCAGTGGTGCATGAAAGCGTGACGCCACACATCACAGCGTGTATGGC 213
Cp 532 AGACTAGCAGGCCAGTGGTGCATGAAAGCGTGACGCCACACATCACAGCGTGTATGGC 473
Db 214 ACCTGTGTGAGGCTGCAGTCCCTGTGTGGCGCGGCACCTCACTCTGGCAGCGCGGTCC 273
Cp 472 ACCTGTGTGAGGCTGCAGTCCCTGTGTGGCGCGGCACCTCACTCTGGCAGCGCGGTCC 413
Db 274 CCCATGCCAGCCATGTTGTCGCCCATACGCGAGTAGTGTGGTCCGGAAGGCCAG 333
Cp 412 CCCATGCCAGCCATGTTGTCGCCCATACGCGAGTAGTGTGGTCCGGAAGGCCAG 353
Db 334 CCAGGCCAGGTAGGGGTAGAGCAGCGGGCGGCAGCGGCTCACCTGGTACAGGCCAC 393
Cp 352 CCAGGCCAGGTAGGGGTAGAGCAGCGGGCGGCAGCGGCTCACCTGGTACAGGCCAC 293
Db 394 GGTACTGGGN-CCGCGCCCGCCACTGACGACGAGAGATCCACCAAGGCCAGCC-ATTTG 451
Cp 292 GGTAGTGGTTCGCCCGCCCGCCACTGACGACGAGAGATCCACCAAGGCCAGCCATTG 233
Db 452 TCGGGCAC-NAAGAAGATGGGGGCCATGCC-AGTTGAGGAGGAGTGCC-AGTGTAG 506
Cp 232 TCGGGCACCAAGAAGATGGGGGCCATGCCAGTTTCAGGGCCAGCTGCCAGTGTAG 175

RESULT 12
LOCUS AA036726 551 bp mRNA EST 10-MAY-1997
DEFINITION 2k30b07.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone
472021 3', similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE
RECEPTOR (HUMAN);, mRNA sequence.
ACCESSION AA036726
NID 91509983
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Euthera; Primates; Catarrhini; Hominiidae;
Homo.
REFERENCE 1 (bases 1 to 551)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le.M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E.,
Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
WashU-Merck EST Project
JOURNAL Unpublished (1995)
TITLE
JOURNAL
COMMENT
Contact: wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the

```

IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 695 Std Error: 0.00
Seq primer: -40ml3 fwd. from Amersham
High quality sequence stop: 321.

FEATURES

source
1. .551
Location/Qualifiers
/organism="Homo sapiens"
/note="Organ: uterus; Vector: pT7T3-Pac; Site_1: Not I;
Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo (dT) primer [5',
AATCGAAGAAATTCGCGCGCCCTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Library
constructed by M. Fatima Bonaudo."
/db_xref="taxon:9606"
/clone="472021"
/clone_lib="Soares pregnant uterus NbHPU"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
complement(<1..>551)
/db_xref="GDB:3758023"
BASE COUNT 123 a 160 c 164 g 96 t 8 others
ORIGIN

Query Match 63.5%; Score 414; DB 5; Length 551;
Best Local Similarity 93.5%; Pred. No. 0.00e+00;
Matches 491; Conservative 0; Mismatches 24; Indels 10; Gaps 10;
Db 30 AATTCATGTTCCAGAACATGCTTAAGCATGCAGAAAGCACAGGACACTGCTCCCGG 89
|||||
Cp 652 AATTCATGTTCCAGAACATGCTTAAGCATGCAGAAAGCACAGGACACTGCTCCCGG 593
Db 90 GTGGGGGCTCAGGTGGGCGCCACTCTGAAGCTCTCTGACCCCTGGGCGAAGGCTG-GAC 148
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Cp 592 GTGGGGGCTCAGGTGGGCGCCACTCTGAAGCTCTCTGACCCCTGGGCGAAGGCGCTGAC 533
Db 149 AGACTAGCAGGCGCCAGTGGTCAATGAAGCGTGACGGCCACCATCACAAAGGCTGATGGC 208
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Cp 532 AGACTAGCAGGCGCCAGTGGTCAATGAAGCGTGACGGCCACCATCACAAAGGCTGATGGC 473
Db 209 ACCTGCTGGT-CAGCTGAGTCCCTGGTGGCGCGGCGCACTCACTCTGGCAGCGC-GTCC 266
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Cp 472 ACCTGCTGGTGGTGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 413
Db 267 CCCAGCGCCAGCCATGGTGTCCCGGCATACGACGAGTAGTTGAGTGTGGTGGTGAAGGCCAG 326
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Cp 412 CCCAGCGCCAGCCATGGTGTCCCGGCATACGACGAGTAGTTGAGTGTGGTGGTGAAGGCCAG 353
Db 327 CCAGCGCANGGTAAGGGGTAGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 386
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Cp 352 CCAGCGCCAGGTA-GGGGTAGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 294
Db 387 CGGTACTGTGANCAGCG 446
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Cp 293 CGGTAGTGGCTGCCCG 235
Db 447 TTGTTGGCGCCACCAAGAAGATGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 506
|||||
Cp 234 T-GT-CGGGCACCAAGAAGATGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 179
Db 507 GTAGAGGCCCGCGGGAACACAGNCTTCTTTTGTGANGCCTTCCA 551
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Cp 178 GTAGAGGCCCGCGGGAACACAGNCTTCTCTGT-GAAGCGCTCCCA 135

RESULT 13
LOCUS AA838533 505 bp mRNA EST 18-MAR-1998
DEFINITION oe39all.s1 NCI-CGAP_Pr25 Homo sapiens cDNA clone IMAGE:1410908
similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR
(HUMAN);, mRNA sequence.

ACCESSION

NID
g2913332
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens

REFERENCE

1 (bases 1 to 505)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

Tissue Procurement: Suzanne L. Topalian, M.D., Robert K. Bright,

Ph.D.

CDNA Library Preparation: Stratagene, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 894 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 323.

FEATURES

source

1. .505
Location/Qualifiers
/organism="Homo sapiens"
/note="Organ: prostate; Vector: Bluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. Normal prostate epithelial cell line (HPV
immortalized). 5' adaptor sequence: 5' GAATTCGCGCAG 3'
3' adaptor sequence: 5' CTCGAGTCTTTTCTTTTCTTTT 3'.
Average insert size: 1.1 kb.
/db_xref="taxon:9606"
/clone="IMAGE:1410908"
/clone_lib="NCI-CGAP_Pr25"
/tissue_type="epithelium (cell line)"
/lab_host="SOLR (kanamycin resistant)"
BASE COUNT 112 a 148 c 156 g 89 t
ORIGIN

Query Match 62.1%; Score 405; DB 16; Length 505;

Best Local Similarity 94.9%; Pred. No. 0.00e+00;

Matches 444; Conservative 0; Mismatches 21; Indels 3; Gaps 3;

Db 41 AATTCATGTTCCAGAACATGCTTAAGCATGCAGAAAGCACAGGACACTGCTCCCGG 100
|||||
Cp 652 AATTCATGTTCCAGAACATGCTTAAGCATGCAGAAAGCACAGGACACTGCTCCCGG 593
Db 101 GTGGGGGCTCAGGTGGGCGCCACTCTGAAGCTCTGTGACCCCTGGGCGAAGGCTTGAC 160
|||||
Cp 592 GTGGGGGCTCAGGTGGGCGCCACTCTGAAGCTCTGTGACCCCTGGGCGAAGGCGCTGAC 533
Db 161 AGACTAGCAGGCGCCAGTGGTCAATGAAGCGTGACGGCCACCATCACAAAGGCTGATGGC 220
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Cp 532 AGACTAGCAGGCGCCAGTGGTCAATGAAGCGTGACGGCCACCATCACAAAGGCTGATGGC 473
Db 221 ACCTGCTGGTGCAGTGCAGTCCCTGGTGGCGCGGCGCACTCACTCTGGCAGCGCGCGTCC 280
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Cp 472 ACCTGCTGGTGCAGTGCAGTCCCTGGTGGCGCGGCGCACTCACTCTGGCAGCGCGCTCC 413
Db 281 CCCAGCGCCAGCCATGGTGTGCCGCCCATACGACGAGTAGTTGAGTGTGGTGGCGAAG-CCAG 339
|||||
Cp 412 CCCAGCGCCAGCCATGGTGTGCCGCCCATACGACGAGTAGTTGAGTGTGGTGGTGAAGGCCAG 353
Db 340 CCAGGCANGGTAGGGGTAGACGACGCGGGCGGC-AGCGGGCTCACCTGGTACCAGGCCAC 398
|||||
Cp 352 CCAGGCANGGTAGGGGTAGACGACGCGGGCGGCACCGGGCTCACCTGGTACCAGGCCAC 293

Db 399 GGTAGTGTCCCGCGCCCGCCACTGAC-AGCAGGAGATCCACCAGGCCCGCCAGCCCATTTG 457
 Cp 292 GGTAGTGTCCCGCGCCCGCCCGCCACTGAC-AGCAGGAGATCCACCAGGCCCGCCAGCCCATTTG 233
 Db 458 TCGGGCACAAGAAGATGGGGGCGCATGGCAAGTTACAGGGCGAGCTG 505
 Cp 232 TCGGGCACAAGAAGATGGGGGCGCATGGCCAGTTACAGGGCGAGCTG 185

RESULT 14
 LOCUS AA805072 543 bp mRNA EST 19-FEB-1998
 DEFINITION OB86C01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1338240
 similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR
 (HUMAN);, mRNA sequence.

ACCESSION AA805072
 NID G2873972
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 543)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert_Strausberg@nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
 Ph.D., Gerald Marti, M.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone Distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html

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 High quality sequence stop: 272.
 Location/Qualifiers
 1. 543
 /organism="Homo sapiens"
 /note="Vector: p7T3D-Pac (Pharmacia) with a modified
 polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was prepared from human tonsillar cells enriched for
 germinal center B cells by flow sorting (CD20+, IgD-),
 provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
 (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
 primed with a Not I - oligo(dT) primer
 [5'-TGTTACCAATCTGAAGTGGAGGCGCGCTCATTTTTTTTTTTTTTTT-
 3']. Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified p7T3 vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M. Fatima Bonaldo."
 /db_xref="taxon:9606"
 /clone="IMAGE:1338240"
 /clone_lib="NCI_CGAP_GCB1"
 /tissue_type="germinal center B cell"
 /lab_host="DH10B"
 122 a 155 c 162 g 104 t

BASE COUNT 122 a 155 c 162 g 104 t
 ORIGIN

Query Match 61.2%; Score 399; DB 15; Length 543;
 Best Local Similarity 94.1%; Pred. No. 0.00e+00;
 Matches 463; Conservative 0; Mismatches 22; Indels 7; Gaps 6;

Db 54 AATTCATGTTCACAGACATGCTTAAGCATGCAGAAAGCACAGGACACTGCTCCCGG 113
 Cp 652 AATTCATGTTCACAGACATGCTTAAGCATGCAGAAAGCACAGGACACTGCTCCCGG 593
 Db 114 GTGGGGCTCAGGTGGGGCCACCTCTGAAGCTCTGTGACCCCTGGGCCAAGCCCTGAC 173
 Cp 592 GTGGGGCTCAGGTGGGGCCACCTCTGAAGCTCTGTGACCCCTGGGCCAAGCCCTGAC 533
 Db 174 AGACTAGCAGGCCAGTGGTGCATGAAGCGTGACGGCCACCATCATCAAGCGTGATGGC 233
 Cp 532 AGACTAGCAGGCCAGTGGTGCATGAAGCGTGACGGCCACCATCATCAAGCGTGATGGC 473
 Db 234 ACCTGCTGTGACAGCTCAGTCCCTGGTGGGGCGGGCAGCTACTCTGGGAGCGCCGCTCC 293
 Cp 472 ACCTGCTGTGACAGCTCAGTCCCTGGTGGGGCGGGCAGCTACTCTGGGAGCGCCGCTCC 413
 Db 294 CCCAGCGCAGCCATGTTGTCGCCCATACGACAGTACTTGTGAGTGGTCTGAAAGGCCAG 353
 Cp 412 CCCAGCGCAGCCATGTTGTCGCCCATACGACAGTACTTGTGAGTGGTCTGAAAGGCCAG 353
 Db 354 CCAGGCCAGTGGGGTAGAGCAGGGCGGGCGCAA-CGGGCTCACCTGTGTACAGGCCAC 412
 Cp 352 CCAGGCCAGTGGGGTAGAGCAGGGCGGGCGGCACGGGGCTCACCTGTGTACAGGCCAC 293
 Db 413 CGTACTTGGGGC-CCGCCCCACTGACACAGAGAGATCCACAAAGCCAGGCCATTTTG 471
 Cp 292 GGTAGTGGCTGCCGCCCGCCACTGACACAGAGAGATCCACAAAGCCAGGCCATTTG 233
 Db 472 TCGG-CAGCAAGAAGATGGGGGCCATGC-AGTTTAAAGCCAGCGGCC-AGTGTAGAG 527
 Cp 232 TCGGGCACAAGAAGATGGGGGCCATGCCAGTTCAGGCCAGCTGCCCGCTGTAGAG 173
 Db 528 GCC-AGGGGAAC 538
 Cp 172 GCCAGGGGAAC 161

RESULT 15
 LOCUS AA768741 507 bp mRNA EST 08-FEB-1998
 DEFINITION OB22901.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:132464
 similar to gb:U12421_cds1 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR
 (HUMAN);, mRNA sequence.

ACCESSION AA768741
 NID G2819456
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 507)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert_Strausberg@nih.gov
 unknown library type
 Insert Length: 612 Std Error: 0.00
 Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 484.
 Location/Qualifiers
 1. 507
 /organism="Homo sapiens"
 /note="Organ: kidney; Vector: p7T3D-Pac (Pharmacia) with
 a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5'-
 AACTGAAGAATTCGGCGCGCAATTTTTTTTTTTTTTTT 3'],
 double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified p7T3 vector. Library
 went through one round of normalization. Library
 constructed by Bento Soares and M. Fatima Bonaldo."
 /db_xref="taxon:9606"

FEATURES
 source

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W P E R L
(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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Distribution rights by Oxford Molecular Ltd
MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Jul 21 14:52:56 1998; Maspar time 7.43 Seconds
Tabular output not generated.
Title: >US-09-047-652A-3
Description: (1-169) from US09047652A.pap
Perfect Score: 1170
Sequence: 1 XXXXXXXXXXXXXXXX.....LNYCVWRDNGWRGRRRLPE 169
Scoring table: PAM 150
Gap 11
Searched: 124785 seqs, 15338987 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: a-geneseq1-2
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27
Statistics: Mean 31.057; Variance 140.986; scale 0.220
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES				Pred. No.	
Result	Query	Length	DB	Description	
No.	Score	Match	ID		
1	100	8.5	483 20	W12136 Alpha-amylase variant	5.89e+00
2	100	8.5	483 20	W12143 Alpha-amylase variant	5.89e+00
3	100	8.5	483 20	W12137 Alpha-amylase variant	5.89e+00
4	100	8.5	483 20	W12138 Alpha-amylase variant	5.89e+00
5	100	8.5	483 20	W12139 Alpha-amylase variant	5.89e+00
6	100	8.5	483 20	W12140 Alpha-amylase variant	5.89e+00
7	100	8.5	483 20	W12115 Alpha-amylase variant	5.89e+00
8	100	8.5	483 20	W12116 Alpha-amylase variant	5.89e+00
9	100	8.5	483 20	W12134 Alpha-amylase variant	5.89e+00
10	100	8.5	483 20	W12133 Alpha-amylase variant	5.89e+00
11	100	8.5	485 27	W31500 Bacillus sp. alpha am	5.89e+00
12	100	8.5	485 27	W31499 Bacillus sp. alpha am	5.89e+00
13	100	8.5	485 20	W12130 Alpha-amylase variant	5.89e+00
14	100	8.5	485 20	W12131 Alpha-amylase variant	5.89e+00
15	100	8.5	485 16	R81835 Bacillus sp. alkaline	5.89e+00
16	100	8.5	485 20	W12127 Alpha-amylase variant	5.89e+00
17	100	8.5	485 20	W12125 Alpha-amylase variant	5.89e+00
18	100	8.5	485 20	W12144 Alpha-amylase variant	5.89e+00
19	100	8.5	485 20	W12110 Alpha-amylase variant	5.89e+00

ALIGNMENTS			
RESULT 1			
ID			
AC	W12136 standard; protein; 483 AA.		
DT	08-APR-1997 (first entry)		
DE	Alpha-amylase variant L351C+M430C+Y243F+delta183+delta184+Q391E+K440Q.		
KW	Alpha-amylase; detergent; thermal stability; oxidation stability; enzyme;		
KW	calcium ion dependency; alpha-amylolytic activity; washing composition;		
KW	textile desizing; papermaking; beer-making; ethanol production;		
KW	sweetener.		
OS	Synthetic.		
FH	Key	Location/Qualifiers	
FT	misc_difference 243	/label= Y243F	
FT	misc_difference 351	/label= L351C	
FT	misc_difference 391	/label= Q391E	
FT	misc_difference 430	/label= M430C	
FT	misc_difference 444	/label= K440Q	
PN	W09623873-A1.		
PD	08-AUG-1996.		
PF	05-FEB-1996; DK00056.		
PR	03-FEB-1995; DK-000126.		
PR	29-MAR-1995; DK-000336.		
PR	29-SEP-1995; DK-001097.		
PR	06-OCT-1995; DK-001121.		
PA	(NOVO) NOVO-NORDISK AS.		
PI	Bisgard-frantzen H, Borchert T, Svendsen A;		
DR	WPI; 96-371423/37.		
PT	Alpha-amylase variants - with improved thermal and oxidation		
PS	stability and reduced calcium ion dependency		
CC	Example 2; ; il1pp; English.		
CC	W12098-W12144 represent alpha-amylase variants of the invention. The		
CC	variants of the invention were created using site directed, or random,		
CC	mutagenesis of the DNA sequences encoding the parent alpha-amylases		
CC	represented by W12955, W12956, R81835 and R81836. W12098-W12136, W12141,		
CC	W12142 and W12144 are specifically variants of the alkaliphilic Bacillus		
CC	strain NCIB 12512 alpha-amylase shown in R81835. These variants can have		
CC	improved thermal stability (such as at temperatures in the range of 40-70		
CC	degrees Celsius), and/or oxidation stability, and/or reduced calcium ion		
CC	dependency. The variants can also have increased alpha-amylolytic		

CC activity (especially at pH values in the range of 8.5-10.5), and improved
 CC binding of a particular substrate. These variant alpha-amylases also
 CC possess improved specificity to a particular substrate, and/or improved
 CC specificity with respect to cleavage of substrate. These sequences can
 CC be used in detergent and washing compositions, and for textile desizing.
 CC The alpha-amylase variants can also be used in papermaking and
 CC beer-making processes. These variants can also be used in the production
 CC of sweeteners and ethanol from starch.
 CC Sequence 483 AA;

Query Match 8.5%; Score 100; DB 20; Length 483;
 Best Local Similarity 40.0%; Pred. No. 5.89e+00;
 Matches 14; Conservative 8; Mismatches 10; Indels 3; Gaps 3;

Db 43 wi-ppawkgtsqndvggyaydly-dlgefndqktv 75
 QY 47 WVLGPVW-GTLYSANGYGSYLWVKELGFGTEKAVV 80

RESULT 2

ID W12143 standard; protein; 483 AA.

AC W12143;
 DT 08-APR-1997 (first entry)
 DE Alpha-amylase variant delta182 + delta184.
 KW Alpha-amylase; detergent; thermal stability; oxidation stability; enzyme;
 KW calcium ion dependency; alpha-amylolytic activity; washing composition;
 KW textile desizing; papermaking; beer-making; ethanol production;
 KW sweetener.
 OS Synthetic.
 PN W09623873-A1.
 PD 08-AUG-1996.
 PF 05-FEB-1996; DK00056.
 PR 03-FEB-1995; DK-000126.
 PR 29-MAR-1995; DK-000336.
 PR 29-SEP-1995; DK-001097.
 PR 06-OCT-1995; DK-001121.
 PA (NOVO) NOVO-NORDISK AS.
 PI Bisgard-frantzen H, Borchert T, Svendsen A;
 DR WPI: 96-371423/37.
 PT Alpha-amylase variants - with improved thermal and oxidation
 PT stability and reduced calcium ion dependency
 PS Example 2; ; ilpp; English.

CC W12098-W12144 represent alpha-amylase variants of the invention. The
 CC variants of the invention were created using site directed, or random,
 CC mutagenesis of the DNA sequences encoding the parent alpha-amylases
 CC represented by W12955, W12956, R81835 and R81836. W12137-W12140, and
 CC W12143 are specifically variants of the alkaphilic Bacillus strain NCIB
 CC 12513 alpha-amylase shown in R81836. These variants can have improved
 CC thermal stability (such as at temperatures in the range of 40-70 degrees
 CC Celsius), and/or oxidation stability, and/or reduced calcium ion
 CC dependency. The variants can also have increased alpha-amylolytic
 CC activity (especially at pH values in the range of 8.5-10.5), and improved
 CC binding of a particular substrate. These variant alpha-amylases also
 CC possess improved specificity to a particular substrate, and/or improved
 CC specificity with respect to cleavage of substrate. These sequences can
 CC be used in detergent and washing compositions, and for textile desizing.
 CC The alpha-amylase variants can also be used in papermaking and
 CC beer-making processes. These variants can also be used in the production
 CC of sweeteners and ethanol from starch.
 CC Sequence 483 AA;

Query Match 8.5%; Score 100; DB 20; Length 483;
 Best Local Similarity 40.0%; Pred. No. 5.89e+00;
 Matches 14; Conservative 8; Mismatches 10; Indels 3; Gaps 3;

Db 43 wi-ppawkgtsqndvggyaydly-dlgefndqktv 75
 QY 47 WVLGPVW-GTLYSANGYGSYLWVKELGFGTEKAVV 80

RESULT 3

ID W12137 standard; protein; 483 AA.

AC W12137;

DT 08-APR-1997 (first entry)
 DE Alpha-amylase variant delta183 + delta184.
 KW Alpha-amylase; detergent; thermal stability; oxidation stability; enzyme;
 KW calcium ion dependency; alpha-amylolytic activity; washing composition;
 KW textile desizing; papermaking; beer-making; ethanol production;
 KW sweetener.
 OS Synthetic.
 PN W09623873-A1.
 PD 08-AUG-1996.
 PF 05-FEB-1996; DK00056.
 PR 03-FEB-1995; DK-000126.
 PR 29-MAR-1995; DK-000336.
 PR 29-SEP-1995; DK-001097.
 PR 06-OCT-1995; DK-001121.
 PA (NOVO) NOVO-NORDISK AS.
 PI Bisgard-frantzen H, Borchert T, Svendsen A;
 DR WPI: 96-371423/37.
 PT Alpha-amylase variants - with improved thermal and oxidation
 PT stability and reduced calcium ion dependency
 PS Example 2; ; ilpp; English.

CC W12098-W12144 represent alpha-amylase variants of the invention. The
 CC variants of the invention were created using site directed, or random,
 CC mutagenesis of the DNA sequences encoding the parent alpha-amylases
 CC represented by W12955, W12956, R81835 and R81836. W12137-W12140, and
 CC W12143 are specifically variants of the alkaphilic Bacillus strain NCIB
 CC 12513 alpha-amylase shown in R81836. These variants can have improved
 CC thermal stability (such as at temperatures in the range of 40-70 degrees
 CC Celsius), and/or oxidation stability, and/or reduced calcium ion
 CC dependency. The variants can also have increased alpha-amylolytic
 CC activity (especially at pH values in the range of 8.5-10.5), and improved
 CC binding of a particular substrate. These variant alpha-amylases also
 CC possess improved specificity to a particular substrate, and/or improved
 CC specificity with respect to cleavage of substrate. These sequences can
 CC be used in detergent and washing compositions, and for textile desizing.
 CC The alpha-amylase variants can also be used in papermaking and
 CC beer-making processes. These variants can also be used in the production
 CC of sweeteners and ethanol from starch.
 CC Sequence 483 AA;

Query Match 8.5%; Score 100; DB 20; Length 483;
 Best Local Similarity 40.0%; Pred. No. 5.89e+00;
 Matches 14; Conservative 8; Mismatches 10; Indels 3; Gaps 3;

Db 43 wi-ppawkgtsqndvggyaydly-dlgefndqktv 75
 QY 47 WVLGPVW-GTLYSANGYGSYLWVKELGFGTEKAVV 80

RESULT 4

ID W12138 standard; protein; 483 AA.

AC W12138;
 DT 08-APR-1997 (first entry)
 DE Alpha-amylase variant delta181 + delta183.
 KW Alpha-amylase; detergent; thermal stability; oxidation stability; enzyme;
 KW calcium ion dependency; alpha-amylolytic activity; washing composition;
 KW textile desizing; papermaking; beer-making; ethanol production;
 KW sweetener.
 OS Synthetic.
 PN W09623873-A1.
 PD 08-AUG-1996.
 PF 05-FEB-1996; DK00056.
 PR 03-FEB-1995; DK-000126.
 PR 29-MAR-1995; DK-000336.
 PR 29-SEP-1995; DK-001097.
 PR 06-OCT-1995; DK-001121.
 PA (NOVO) NOVO-NORDISK AS.
 PI Bisgard-frantzen H, Borchert T, Svendsen A;
 DR WPI: 96-371423/37.
 PT Alpha-amylase variants - with improved thermal and oxidation
 PT stability and reduced calcium ion dependency
 PS Example 2; ; ilpp; English.

CC W12098-W12144 represent alpha-amylase variants of the invention. The
 CC variants of the invention were created using site directed, or random,
 CC mutagenesis of the DNA sequences encoding the parent alpha-amylases
 CC represented by W12955, W12956, R81835 and R81836. W12137-W12140, and
 CC W12143 are specifically variants of the alkaphilic Bacillus strain NCIB
 CC 12513 alpha-amylase shown in R81836. These variants can have improved
 CC thermal stability (such as at temperatures in the range of 40-70 degrees
 CC Celsius), and/or oxidation stability, and/or reduced calcium ion
 CC dependency. The variants can also have increased alpha-amylolytic
 CC activity (especially at pH values in the range of 8.5-10.5), and improved
 CC binding of a particular substrate. These variant alpha-amylases also
 CC possess improved specificity to a particular substrate, and/or improved
 CC specificity with respect to cleavage of substrate. These sequences can
 CC be used in detergent and washing compositions, and for textile desizing.
 CC The alpha-amylase variants can also be used in papermaking and
 CC beer-making processes. These variants can also be used in the production
 CC of sweeteners and ethanol from starch.
 CC Sequence 483 AA;

Query Match 8.5%; Score 100; DB 20; Length 483;
 Best Local Similarity 40.0%; Pred. No. 5.89e+00;
 Matches 14; Conservative 8; Mismatches 10; Indels 3; Gaps 3;

Db 43 wi-ppawkgtsqndvggyaydly-dlgefndqktv 75
 QY 47 WVLGPVW-GTLYSANGYGSYLWVKELGFGTEKAVV 80

RESULT 3

ID W12137 standard; protein; 483 AA.

AC W12137;

PR 29-SEP-1995; DK-001097.
 PR 06-OCT-1995; DK-001121.
 PA (NOVO) NOVO-NORDISK AS.
 PI Bisgard-frantzen H, Borchert T, Svendsen A;
 DR WPI; 96-371423/37.
 PT Alpha-amylase variants - with improved thermal and oxidation
 PT stability and reduced calcium ion dependency
 PS Claim 9; ; ilpp: English.
 CC W12098-W12144 represent alpha-amylase variants of the invention. The
 CC variants of the invention were created using site directed, or random,
 CC mutagenesis of the DNA sequences encoding the parent alpha-amylases
 CC represented by W12955, W12956, R81835 and R81836. W12098-W12136, W12141,
 CC W12142 and W12144 are specifically variants of the alkaliphilic Bacillus
 CC strain NCIB 12512 alpha-amylase shown in R81835. These variants can have
 CC improved thermal stability (such as at temperatures in the range of 40-70
 CC degrees Celsius), and/or oxidation stability, and/or reduced calcium ion
 CC dependency. The variants can also have increased alpha-amylolytic
 CC activity (especially at pH values in the range of 8.5-10.5), and improved
 CC binding of a particular substrate. These variant alpha-amylases also
 CC possess improved specificity to a particular substrate, and/or improved
 CC specificity with respect to cleavage of substrate, and/or improved
 CC be used in detergent and washing compositions, and for textile desizing.
 CC The alpha-amylase variants can also be used in papermaking and
 CC beer-making processes. These variants can also be used in the production
 CC of sweeteners and ethanol from starch.
 CC Sequence 483 AA;
 SQ

Query Match 8.5%; Score 100; DB 20; Length 483;
 Best Local Similarity 40.0%; Pred. No. 5.89e+00;
 Matches 14; Conservative 8; Mismatches 10; Indels 3; Gaps 3;
 Db 43 w1-ppawkgtsqndvgvgaydly-dlgefnkgkv 75
 QY 47 WVLGPVW-GTLYSANGYGSYLWVKELGGFTKAVV 80

RESULT 8
 ID W12116 standard; protein; 483 AA.
 AC W12116;
 DT 08-APR-1997 (first entry)
 DE Alpha-amylase variant delta183 + delta184.
 KW Alpha-amylase; detergent; thermal stability; oxidation stability; enzyme;
 KW calcium ion dependency; alpha-amylolytic activity; washing composition;
 KW textile desizing; papermaking; beer-making; ethanol production;
 KW sweetener.
 OS Synthetic.
 PN W09623873-Al.
 PD 08-AUG-1996.
 PF 05-FEB-1996; DK0056.
 PR 03-FEB-1995; DK-000126.
 PR 29-MAR-1995; DK-000336.
 PR 29-SEP-1995; DK-001097.
 PR 06-OCT-1995; DK-001121.
 PA (NOVO) NOVO-NORDISK AS.
 PI Bisgard-frantzen H, Borchert T, Svendsen A;
 DR WPI; 96-371423/37.
 PT Alpha-amylase variants - with improved thermal and oxidation
 PT stability and reduced calcium ion dependency
 PS Claim 9; ; ilpp: English.
 CC W12098-W12144 represent alpha-amylase variants of the invention. The
 CC variants of the invention were created using site directed, or random,
 CC mutagenesis of the DNA sequences encoding the parent alpha-amylases
 CC represented by W12955, W12956, R81835 and R81836. W12098-W12136, W12141,
 CC W12142 and W12144 are specifically variants of the alkaliphilic Bacillus
 CC strain NCIB 12512 alpha-amylase shown in R81835. These variants can have
 CC improved thermal stability (such as at temperatures in the range of 40-70
 CC degrees Celsius), and/or oxidation stability, and/or reduced calcium ion
 CC dependency. The variants can also have increased alpha-amylolytic
 CC activity (especially at pH values in the range of 8.5-10.5), and improved
 CC binding of a particular substrate. These variant alpha-amylases also
 CC possess improved specificity to a particular substrate, and/or improved
 CC specificity with respect to cleavage of substrate, and/or improved
 CC be used in detergent and washing compositions, and for textile desizing.
 CC

CC The alpha-amylase variants can also be used in papermaking and
 CC beer-making processes. These variants can also be used in the production
 CC of sweeteners and ethanol from starch.
 CC Sequence 483 AA;
 SQ

Query Match 8.5%; Score 100; DB 20; Length 483;
 Best Local Similarity 40.0%; Pred. No. 5.89e+00;
 Matches 14; Conservative 8; Mismatches 10; Indels 3; Gaps 3;
 Db 43 w1-ppawkgtsqndvgvgaydly-dlgefnkgkv 75
 QY 47 WVLGPVW-GTLYSANGYGSYLWVKELGGFTKAVV 80

RESULT 9
 ID W12134 standard; protein; 483 AA.
 AC W12134;
 DT 08-APR-1997 (first entry)
 DE Alpha-amylase variant L351C + M430C + delta183 + delta184.
 KW Alpha-amylase; detergent; thermal stability; oxidation stability; enzyme;
 KW calcium ion dependency; alpha-amylolytic activity; washing composition;
 KW textile desizing; papermaking; beer-making; ethanol production;
 KW sweetener.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT misc_difference 351 /label= L351C
 FT misc_difference 430 /label= M430C
 FT W09623873-Al.
 PN 08-AUG-1996.
 PD 05-FEB-1996; DK0056.
 PR 03-FEB-1995; DK-000126.
 PR 29-MAR-1995; DK-000336.
 PR 29-SEP-1995; DK-001097.
 PR 06-OCT-1995; DK-001121.
 PA (NOVO) NOVO-NORDISK AS.
 PI Bisgard-frantzen H, Borchert T, Svendsen A;
 DR WPI; 96-371423/37.
 PT Alpha-amylase variants - with improved thermal and oxidation
 PT stability and reduced calcium ion dependency
 PS Example 2; ; ilpp: English.
 CC W12098-W12144 represent alpha-amylase variants of the invention. The
 CC variants of the invention were created using site directed, or random,
 CC mutagenesis of the DNA sequences encoding the parent alpha-amylases
 CC represented by W12955, W12956, R81835 and R81836. W12098-W12136, W12141,
 CC W12142 and W12144 are specifically variants of the alkaliphilic Bacillus
 CC strain NCIB 12512 alpha-amylase shown in R81835. These variants can have
 CC improved thermal stability (such as at temperatures in the range of 40-70
 CC degrees Celsius), and/or oxidation stability, and/or reduced calcium ion
 CC dependency. The variants can also have increased alpha-amylolytic
 CC activity (especially at pH values in the range of 8.5-10.5), and improved
 CC binding of a particular substrate. These variant alpha-amylases also
 CC possess improved specificity to a particular substrate, and/or improved
 CC specificity with respect to cleavage of substrate, and/or improved
 CC be used in detergent and washing compositions, and for textile desizing.
 CC The alpha-amylase variants can also be used in papermaking and
 CC beer-making processes. These variants can also be used in the production
 CC of sweeteners and ethanol from starch.
 CC Sequence 483 AA;
 SQ

Query Match 8.5%; Score 100; DB 20; Length 483;
 Best Local Similarity 40.0%; Pred. No. 5.89e+00;
 Matches 14; Conservative 8; Mismatches 10; Indels 3; Gaps 3;
 Db 43 w1-ppawkgtsqndvgvgaydly-dlgefnkgkv 75
 QY 47 WVLGPVW-GTLYSANGYGSYLWVKELGGFTKAVV 80

RESULT 10
 ID W12133 standard; protein; 483 AA.
 AC W12133;
 DT 08-APR-1997 (first entry)
 DE Alpha-amylase variant L351C + M430C + delta183 + delta184.
 KW Alpha-amylase; detergent; thermal stability; oxidation stability; enzyme;
 KW calcium ion dependency; alpha-amylolytic activity; washing composition;
 KW textile desizing; papermaking; beer-making; ethanol production;
 KW sweetener.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT misc_difference 351 /label= L351C
 FT misc_difference 430 /label= M430C
 FT W09623873-Al.
 PN 08-AUG-1996.
 PD 05-FEB-1996; DK0056.
 PR 03-FEB-1995; DK-000126.
 PR 29-MAR-1995; DK-000336.
 PR 29-SEP-1995; DK-001097.
 PR 06-OCT-1995; DK-001121.
 PA (NOVO) NOVO-NORDISK AS.
 PI Bisgard-frantzen H, Borchert T, Svendsen A;
 DR WPI; 96-371423/37.
 PT Alpha-amylase variants - with improved thermal and oxidation
 PT stability and reduced calcium ion dependency
 PS Example 2; ; ilpp: English.
 CC W12098-W12144 represent alpha-amylase variants of the invention. The
 CC variants of the invention were created using site directed, or random,
 CC mutagenesis of the DNA sequences encoding the parent alpha-amylases
 CC represented by W12955, W12956, R81835 and R81836. W12098-W12136, W12141,
 CC W12142 and W12144 are specifically variants of the alkaliphilic Bacillus
 CC strain NCIB 12512 alpha-amylase shown in R81835. These variants can have
 CC improved thermal stability (such as at temperatures in the range of 40-70
 CC degrees Celsius), and/or oxidation stability, and/or reduced calcium ion
 CC dependency. The variants can also have increased alpha-amylolytic
 CC activity (especially at pH values in the range of 8.5-10.5), and improved
 CC binding of a particular substrate. These variant alpha-amylases also
 CC possess improved specificity to a particular substrate, and/or improved
 CC specificity with respect to cleavage of substrate, and/or improved
 CC be used in detergent and washing compositions, and for textile desizing.
 CC

(TM)

Result No.	Query			DB	ID	Description	Pred. No.
	Score	Match	Length				
1	1160	99.1	169	2	S14257	benzodiazepine recept	3.12e-17
2	1008	86.2	169	2	I57993	peripheral-type benzo	1.75e-14
3	1000	85.5	169	2	JC1393	benzodiazepine recept	3.93e-14
4	995	85.0	169	2	A53405	peripheral-type benzo	2.75e-14
5	956	81.7	169	2	I38105	peripheral benzodiazepine	1.04e-13
6	944	80.7	169	2	A39473	peripheral-type benzo	1.10e-13
7	339	29.0	160	2	S04404	crk protein - Rhodob	2.20e-34
8	327	27.9	153	2	B69434	benzodiazepine recept	1.60e-32
9	307	26.2	158	2	A57438	tryptophan-rich senso	1.94e-29
10	291	24.9	157	2	S49632	crk protein - Rhodob	5.41e-27
11	211	18.0	31	2	I48082	mitochondrial benzodi	3.98e-15
12	160	13.7	155	2	G69987	hypothetical protein	4.83e-08
13	130	11.1	159	2	S76477	hypothetical protein	3.58e-04
14	115	9.8	283	2	S45776	peptide transport prot	2.33e-02
15	105	9.0	239	2	C47755	serine enzyme secreti	3.28e-01
16	105	9.0	634	2	S75982	hypothetical protein	3.28e-01
17	102	8.7	188	2	S70680	bpiJ protein - Bordet	7.08e-01
18	102	8.7	285	2	S77220	hypothetical protein	7.08e-01
19	101	8.6	246	2	D64800	glutamate/aspartate t	9.12e-01
20	100	8.5	292	2	G59897	conserved hypothetical	1.17e+00
21	100	8.5	368	2	A45831	MHC class I histocomp	1.17e+00
22	100	8.5	418	2	A64783	hypothetical protein	1.17e+00
23	97	8.3	271	2	JC47832	phosphatidate cytidyl	2.48e+00

```
#authors      Garnier, M.; Dimchev, A.B.; Boujrad, N.; Price, J.M.; Musto,
#journal      N.A.; Papadopoulos, V
#title        Mol. Pharmacol. (1994) 45:201-211
#cross-references MUID:94158796
#accession    I57953
#status       preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues     1-169 #label RES
#cross-references GB:L17306; NID:g309441; PID:g309442
#length 169 #molecular-weight 18841 #checksum 4647
SUMMARY
Query Match      86.2%; Score 1008; DB 2; Length 169;
Best Local Similarity 84.6%; Pred. No. 1.75e-144;
Matches 121; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

Db 27 RGEGLRWASLQKPSWHPRTWLPIWGTLYSAMGYGYVWVKELGGFTEDAMVPLGLYT 86
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 27 HGEGLRWYAGLQKPSWHPHVLGPGVWGTLYSAMGYGYVWVKELGGFTAKAVPLGLYT 86
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 87 GOLALNWAHPPIFFGARQMGWALDVLVSGVATATTALWHRVSPPAARLLYPYLAWLAF 146
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 87 GOLALNWAHPPIFFGARQMGWALDVLVSGAATAATVAVYQVSPLAARLLYPYLAWLAF 146
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 147 ATVLNYYVWRDNRGGRGSRLE 169
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 147 TTTLNVCVRDNRHGWGRRRLPE 169
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3
ENTRY      JC1393 #type complete
TITLE      benzodiazepine receptor, mitochondrial - rat
ALTERNATE_NAMES benzodiazepine receptor, PKBS
ORGANISM    peripheral-type benzodiazepine receptor
DATE        30-Sep-1993 #sequence-revision 30-Sep-1993 #text_change
10-Sep-1997
ACCESSIONS  JC1393; A32680
REFERENCE    JC1393
#authors     Casalotti, S.O.; Palaia, G.; Yakovlev, A.G.; Csikos, T.;
#journal     Grayson, D.R.; Krueger, K.E.
#title       Structure of the rat gene encoding the mitochondrial
benzodiazepine receptor.
#accession   JC1393
#molecule_type DNA
#residues    1-169 #label CAS
#cross-references GB:M64221; NID:g206478; PID:g206480; GB:M95864
REFERENCE    A32680
#authors     Sprengel, R.; Werner, P.; Seeburg, P.H.; Mukhin, A.G.; Santi,
#journal     M.R.; Grayson, D.R.; Guidotti, A.; Krueger, K.E.
#title       J. Biol. Chem. (1989) 264:20415-20421
Molecular cloning and expression of cDNA encoding a
peripheral-type benzodiazepine receptor.
#cross-references MUID:90062173
#accession   A32680
#molecule_type mRNA
#residues    1-169 #label SPR
#cross-references GB:J05122; NID:g206161; PID:g206162
COMMENT      This protein is located mainly in the mitochondrial outer membrane.
GENETICS
#gene        MBR
#introns     61/2; 107/3
#exons       61/2; 107/3
KEYWORDS     mitochondrial; receptor; transmembrane protein
FEATURE
6-26         #domain transmembrane #status predicted #label TM1\
47-67         #domain transmembrane #status predicted #label TM2\
80-100        #domain transmembrane #status predicted #label TM3\
106-126       #domain transmembrane #status predicted #label TM4\
135-155       #domain transmembrane #status predicted #label TM5
SUMMARY      #length 169 #molecular-weight 18940 #checksum 5649

Query Match      85.5%; Score 1000; DB 2; Length 169;
Best Local Similarity 83.2%; Pred. No. 2.75e-142;
Matches 119; Conservative 14; Mismatches 10; Indels 0; Gaps 0;

Db 27 RGEGLRWASLQKPSWHPRTWLPIWGTLYSAMGYGYVWVKELGGFTEDAMVPLGLYT 86
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 27 HGEGLRWYAGLQKPSWHPHVLGPGVWGTLYSAMGYGYVWVKELGGFTAKAVPLGLYT 86
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 87 GOLALNWAHPPIFFGARQMGWALDVLVSGVATATTALWHRVSPPAARLLYPYLAWLAF 146
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 87 GOLALNWAHPPIFFGARQMGWALDVLVSGAATAATVAVYQVSPLAARLLYPYLAWLAF 146
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 147 ATVLNYYVWRDNRGGRGSRLE 169
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 147 TTTLNVCVRDNRHGWGRRRLPE 169
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
ENTRY      A53405 #type complete
TITLE      peripheral-type benzodiazepine receptor 1
ALTERNATE_NAMES isoquinoline-binding protein - mouse
ORGANISM    peripheral-type benzodiazepine receptor
DATE        12-May-1994 #sequence-revision 12-May-1994 #text_change
10-Sep-1997
ACCESSIONS  A53405; I55415; I49099
REFERENCE    A53405
#authors     Taketani, S.; Kohno, H.; Okuda, M.; Furukawa, T.; Tokunaga,
#journal     J. Biol. Chem. (1994) 269:7527-7531
#title       Induction of peripheral-type benzodiazepine receptors during
differentiation of mouse erythroleukemia cells. A possible
involvement of these receptors in heme biosynthesis.
#accession   A53405
#status       preliminary; not compared with conceptual translation
#molecule_type mRNA
#residues     1-169 #label TAK
#cross-references GB:D21207; NID:g484053; PID:d1005281; PID:g484054
155415
REFERENCE    Taketani, S.; Kohno, H.; Okuda, M.; Furukawa, T.; Tokunaga,
#authors     J. Biol. Chem. (1994) 269:2527-7531
#journal     Induction of peripheral-type benzodiazepine receptors during
differentiation of mouse erythroleukemia cells. A possible
involvement of these receptors in heme biosynthesis.
#accession   I55415
#status       preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues     1-169 #label RES
#cross-references GB:D21207; NID:g484053; PID:g484054
138724
REFERENCE    Yakovlev, A.G.; Ruffo, M.; Jurka, J.; Krueger, K.E.
#authors     Gene (1995) 155:201-205
#journal     Comparison of repetitive elements in the third intron of
human and rodent mitochondrial benzodiazepine
receptor-encoding genes.
#cross-references MUID:95237610
#accession   I49099
#status       preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues     95-125 #label RE2
#cross-references EMBL:U12419; NID:g529941; PID:g529942
GENETICS
#gene        MBR
#introns     107/3
#exons       107/3
KEYWORDS     mitochondrial
SUMMARY      #length 169 #molecular-weight 18829 #checksum 3513

Query Match      85.0%; Score 995; DB 2; Length 169;
Best Local Similarity 83.2%; Pred. No. 2.75e-142;
Matches 119; Conservative 14; Mismatches 10; Indels 0; Gaps 0;

Db 27 RGEGLRWASLQKPSWHPRTWLPIWGTLYSAMGYGYVWVKELGGFTEDAMVPLGLYT 86
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 27 HGEGLRWYAGLQKPSWHPHVLGPGVWGTLYSAMGYGYVWVKELGGFTAKAVPLGLYT 86
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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Db 87 GOLALNANWPPPIFFGARQMGWALADLLLVSGVATATTAWHRVSPPAARLLYPYLAWLAF 146
|||||
QY 87 GOLALNANWPPPIFFGARQMGWALVLLLVSGAAATTVAVYQVSPLAARLLYPYLAWLAF 146
|||||

Db 147 ATVLNYYVNRDNGRGGSLAE 169
:|||||
QY 147 TTTLNVCVWRDNGHGGRRLPE 169
:|||||

RESULT 5
ENTRY I38105 #type complete
TITLE peripheral benzodiazepine receptor - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 24-May-1996 #sequence_revision 24-May-1996 #text_change
04-Oct-1996

ACCESSIONS I38105
REFERENCE A49361
#authors Lin, D.; Chang, Y.J.; Strauss, J.F.; Miller, W.L.
#journal Genomics (1993) 18:643-650
#title The human peripheral benzodiazepine receptor gene: cloning and characterization of alternative splicing in normal tissues and in a patient with congenital lipid adrenal hyperplasia.

#cross-references MUID:94140364
#accession I38105 preliminary; translated from GB/EMBL/DBJ
#status preliminary
#molecule_type DNA
#residues 1-169 #label RES
#cross-references GB:L21954; NID:g483405; PID:g488425

GENETICS
#introns 61/2; 107/3
SUMMARY #length 169 #molecular-weight 18483 #checksum 2466

Query Match 81.7%; Score 956; DB 2; Length 169;
Best Local Similarity 86.2%; Pred. No. 1.04e-135;
Matches 125; Conservative 7; Mismatches 9; Indels 4; Gaps 4;

Db 27 HGEGRLWYAGLQKPSHPHVVLPVWGTLVSAMGYSGYLVNKLGGFTKEKAVSPGPH 86
|||||
QY 27 HGEGRLWYAGLQKPSHPHVVLPVWGTLVSAMGYSGYLVNKLGGFTKEKAVVPLG-LY 85
|||||

Db 87 WAAGPELGHV-PLL-GARQMGWALVLLLVSGAAATTVAVTQVSPLAARLLYPYLAWL 144
::|::|
QY 86 -TQALNANWPPPIFFGARQMGWALVLLLVSGAAATTVAVTQVSPLAARLLYPYLAWL 144
|||

Db 145 AFATTLNVCVWRDNGHGGRRLPE 169
|||
QY 145 AFTTLNVCVWRDNGHGGRRLPE 169
|||

RESULT 6
ENTRY A39473 #type complete
TITLE peripheral-type benzodiazepine receptor/isoquinoline-binding protein - bovine
ORGANISM #formal_name Bos primigenius taurus #common_name cattle
DATE 27-Mar-1992 #sequence_revision 10-Apr-1992 #text_change
10-Sep-1997

ACCESSIONS A39473
REFERENCE A39473
#authors Parola, A.L.; Stump, D.G.; Pepperl, D.J.; Krueger, K.E.; Regan, J.W.; Laird II, H.E.
#journal J. Biol. Chem. (1991) 266:14082-14087
#title Cloning and expression of a pharmacologically unique bovine peripheral-type benzodiazepine receptor isoquinoline binding protein.

#cross-references MUID:91310699
#accession A39473 preliminary
#status preliminary
#molecule_type mRNA
#residues 1-169 #label PAR
#cross-references GB:M64520; NID:g163488; PID:g163489
#note the authors translated the codon GGC for residue 116 as

Ala
transmembrane protein
#length 169 #molecular-weight 18927 #checksum 4766

Query Match 80.7%; Score 944; DB 2; Length 169;
Best Local Similarity 75.5%; Pred. No. 1.10e-133;
Matches 108; Conservative 24; Mismatches 11; Indels 0; Gaps 0;

Db 27 RGEGRWYASLQKPPHPPWILAPIWGTLYSAMGYSGYMIWKLGGFSKEAVVPLGLYA 86
:|||||
QY 27 HGEGLRWYAGLQKPSHPHVVLPVWGTLVSAMGYSGYLVNKLGGFTKEKAVVPLGLYT 86
:|||||

Db 87 GOLALNANWPPPIFFGTROMGVALVLLLTGMAAATAMAHQVSPPAACLLYPYLAWLAF 146
|||||
QY 87 GOLALNANWPPPIFFGARQMGWALVLLLVSGAAATTVAVYQVSPLAARLLYPYLAWLAF 146
|||||

Db 147 AGMLNRYMQRDQVRSRRRLSE 169
:|||||
QY 147 TTTLNVCVWRDNGHGGRRLPE 169
:|||||

RESULT 7
ENTRY S04404 #type complete
TITLE crtk protein Rhodobacter capsulatus
ORGANISM #formal_name Rhodobacter capsulatus
DATE 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change
09-Sep-1997

ACCESSIONS S04404
REFERENCE S04401
#authors Armstrong, G.A.; Alberti, M.; Leach, F.; Hearst, J.E.
#journal Mol. Gen. Genet. (1989) 216:254-268
#title Nucleotide sequence, organization, and nature of the protein products of the carotenoid biosynthesis gene cluster of Rhodobacter capsulatus.

#cross-references MUID:89313663
#accession S04404
#molecule_type DNA
#residues 1-160 #label ARM
#cross-references EMBL:X52291; NID:g45996; PID:g46000

GENETICS
#gene crtk
KEYWORDS transmembrane protein
SUMMARY #length 160 #molecular-weight 17608 #checksum 109

Query Match 29.0%; Score 339; DB 2; Length 160;
Best Local Similarity 37.2%; Pred. No. 2.20e-34;
Matches 48; Conservative 35; Mismatches 43; Indels 3; Gaps 3;

Db 28 WYDSLKKPSWPPNMLFPVAVSTLYLSISAARV-SGLAMENELAVLGAFWAVQIAYN 86
|||
QY 33 WYAGLQKPSHPHVVLPVWGTLVSAMGYSGYLVNKLGGFTKEKAVVPLGLYTQALN 92
|||

Db 87 TLWTPIFFGLHRLAGMLVLLVNLVFTATCVLFSVDWLSG-LMFVPVIVVTYAGALN 145
|
QY 93 WAMPPPIFFGARQMGWALVLLLVSGAAATTVAVYQVSPLAARLLYPYLAWLAF 151
|||

Db 146 FSVWRNLNG 154
:|
QY 152 YCVWRDNGH 160
:|

RESULT 8
ENTRY B69434 #type complete
TITLE benzodiazepine receptor/sensory transduction protein homolog
ORGANISM - Archaeoglobus fulgidus
DATE 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
05-Dec-1997

ACCESSIONS B69434
REFERENCE A89250
#authors Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, R.J.; Gwinn, M.; Hickey, E.K.; Peterson, J.D.; Richardson, D.L.; Kerlavage, A.R.; Graham,

D.E.: Kyrpides, N.C.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Dougherty, B.A.; McKenny, K.; Adams, M.D.; Loftus, B.; Peterson, S.; Reich, C.I.; McNeil, L.K.; Badger, J.H.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.; Utterback, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kalne, B.P.; Sykes, S.M.; Sadow, P.W.; D'Andrea, K.P.; Bowman, C.; Fujii, C.; Garland, S.A.; Mason, T.M.; Olsen, G.J.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Venter, J.C.

#journal Nature (1997) 390:364-370
#title The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon *Archaeoglobus fulgidus*.
#cross-references MIMD:38049343
#accession B69434
#status preliminary: nucleic acid sequence not shown; translation: not shown

#molecule_type DNA
#residues 1-153 #label KLE
#cross-references GB:A6000782; TIGR:AF1475
SUMMARY #length 153 #molecular-weight 17185 #checksum 36

Query Match 27.9%; Score 327; DB 2; Length 153;
Best Local Similarity 39.0%; Pred. No. 1.60e-32;
Matches 48; Conservative 30; Mismatches 39; Indels 6; Gaps 6;

Db 31 WYAGVEKPPFPNNLFGPANTLLYFLIGVLYIAM-E-NGFWNDSRVKATFT-OLGLN 87

QY 33 WYAGLQKPSHPHPPHVLGPVWGTLISAMGYSLVWKELGGFTKAVVPLGLYTGQLALN 92

Db 88 FLMSILFFGQNLPA-GLVDIIADIAVILTYIVYHHSK-ASLLLPGLNGLFASALN 145

QY 93 WAWPPIFFGARQ-MGVALVDLLVSGAAATTVAVIQVSPLAARLLPYLAWLAFTTLN 151

Db 146 FAI 148

QY 152 YCV 154

RESULT 9
ENTRY A57438 #type complete
TITLE tryptophan-rich sensory protein - Rhodobacter sphaeroides (strain 2.4.1)
ORGANISM #formal_name Rhodobacter sphaeroides
DATE 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change

ACCESSIONS A57438
REFERENCE A57438
#authors Yeliseev, A.A.; Kaplan, S
#journal J. Biol. Chem. (1985) 270:21167-21175
#title A sensory transducer homologous to the mammalian peripheral-type benzodiazepine receptor regulates photosynthetic membrane complex formation in Rhodobacter sphaeroides 2.4.1.

#accession A57438
#status preliminary: not compared with conceptual translation
#molecule_type DNA
#residues 1-158 #label YEL

GENETICS tspro
#gene tspro
SUMMARY #length 158 #molecular-weight 17976 #checksum 9469

Query Match 26.2%; Score 307; DB 2; Length 158;
Best Local Similarity 38.3%; Pred. No. 1.94e-29;
Matches 46; Conservative 29; Mismatches 40; Indels 5; Gaps 3;

Db 30 WYDNLKPNWNPFRVPLAWTSLYFLMSLAAMRV-AQLEG-SGQA---LAFYAQLAFN 84

QY 33 WYAGLQKPSHPHPPHVLGPVWGTLISAMGYSLVWKELGGFTKAVVPLGLYTGQLALN 92

Db 85 TLWTPVFFGKRMATLAVVVMVLEVAATMAFFOLDTWAGLVFVPLIWIATATGLNF 144

QY 93 WAWPPIFFGARQMGWALVDLLVSGAAATTVAVIQVSPLAARLLPYLAWLAFTTLN 152

RESULT 10

ENTRY S49622 #type complete

TITLE crtK protein - Rhodobacter sphaeroides

ORGANISM #formal_name Rhodobacter sphaeroides

DATE 05-Mar-1995 #sequence_revision 12-May-1995 #text_change 09-Sep-1997

ACCESSIONS S49622

REFERENCE S49619

#authors Lang, H.P.; Cogdell, R.J.; Takaichi, S.; Hunter, C.N.

#submission submitted to the EMBL Data Library, November 1994

#description The complete DNA sequence, specific TNS insertion map and gene assignment of the carotenoid biosynthesis genes of Rhodobacter sphaeroides.

#accession S49622 preliminary

#status preliminary

#molecule_type DNA

#residues 1-157 #label LAN

#cross-references EMBL:X82458; NID:g575405; PID:g575409

GENETICS

#gene crtK

SUMMARY #length 157 #molecular-weight 17854 #checksum 6363

Query Match 24.9%; Score 291; DB 2; Length 157;
Best Local Similarity 36.7%; Pred. No. 5.41e-27;
Matches 44; Conservative 28; Mismatches 42; Indels 6; Gaps 5;

Db 30 WYDNLKPNWNPFRVPLAWTSLYFLMSLAPC-GWR--SS-KVRAGAGL-LCA-QLAFN 83

QY 33 WYAGLQKPSHPHPPHVLGPVWGTLISAMGYSLVWKELGGFTKAVVPLGLYTGQLALN 92

Db 84 TLWTPVFFGKRMATLAVVVMVLEVAATMAFFOLDTWAGLVFVPLIWIATATGLNF 143

QY 93 WAWPPIFFGARQMGWALVDLLVSGAAATTVAVIQVSPLAARLLPYLAWLAFTTLN 152

RESULT 11
ENTRY I48082 #type fragment
TITLE mitochondrial benzodiazepine receptor - Chinese hamster (fragment)

ORGANISM #formal_name Cricetulus griseus #common_name Chinese hamster

DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 28-Feb-1997

ACCESSIONS I48082

REFERENCE I38724

#authors Yakovlev, A.G.; Ruffo, M.; Jurka, J.; Krueger, K.E.

#journal Gene (1995) 155:201-205

#title Comparison of repetitive elements in the third intron of human and rodent mitochondrial benzodiazepine receptor-encoding genes.

#cross-references MIMD:95237610

#accession I48082 preliminary: translated from GB/EMBL/DBJ

#status preliminary

#molecule_type DNA

#residues 1-31 #label RES

#cross-references EMBL:U12420; NID:g529943; PID:g1039378

GENETICS

#gene MBR

#introns 13/3

KEYWORDS mitochondrial

SUMMARY #length 31 #checksum 7498

Query Match 18.0%; Score 211; DB 2; Length 31;
Best Local Similarity 87.1%; Pred. No. 3.98e-15;
Matches 27; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 1 WPTIFFGARQMGWALADLLVSGVATATTLA 31

QY 95 WPTIFFGARQMGWALVDLLVSGAAATTVAA 125

RESULT 12


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ENTRY      G69987      #type complete
TITLE      hypothetical protein ytaB - Bacillus subtilis
ORGANISM   Bacillus subtilis
DATE       05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
ACCESSIONS G69987
REFERENCE   A69580
#authors   Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.;
            Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.;
            Bolotin, A.; Borchert, S.; Boriss, R.G.; Boursier, L.; Brans,
            A.; Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.;
            Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
            Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.;
            Daniel, R.A.; Denizot, F.; Devine, K.M.; Dueterhoeft, A.;
            Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.;
            Fabret, C.; Ferrari, E.; Foulger, D.; Fritz, C.; Fujita,
            M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleron, N.; Ghm,
            S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandi, G.;
            Guiseppi, G.; Guy, B.J.; Hega, K.; Halech, J.; Harwood,
            C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.;
            Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.;
            Kasahara, Y.; Klaerr-Blanchard, M.; Klein, C.; Kobayashi,
            Y.; Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.;
            Kurita, K.; Lapidus, A.; Lardinois, S.; Lauber, J.;
            Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.;
            Maueel, C.; Medigue, C.; Medina, N.; Mellado, R.P.; Mizuno,
            M.; Moestl, D.; Nakai, S.; Noback, M.; Noone, D.; O'Reilly,
            M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro,
            V.; Pohl, T.M.; Portetelle, D.; Porwolik, S.; Prescott,
            A.M.; Presecan, E.; Pujic, P.; Purnelle, B.; Rapoport, G.;
            Rey, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.;
            Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, E.;
            Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.;
            Sekowska, A.; Serror, S.J.; Serror, P.; Shin, B.S.; Soldo,
            B.; Sorokin, A.; Tacconi, E.; Takagi, T.; Takahashi, H.;
            Takemaru, K.; Takeuchi, M.; Tanakoshi, A.; Tanaka, T.;
            Terpstra, P.; Tognoni, A.; Tosato, V.; Uchlyama, S.;
            Vandenberg, M.; Vannier, F.; Vassarotti, A.; Viari, A.;
            Wambutt, R.; Wedler, E.; Wedler, H.; Weitzenecker, T.;
            Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto,
            K.; Yata, K.; Yoshida, K.; Yoshikawa, H.F.; Zumstein, E.;
            Yoshikawa, H.; Danchin, A.
#journal   Nature (1997) 390:249-256
#title     The complete genome sequence of the Gram-positive bacterium
            Bacillus subtilis.
#accession G69987
#status    preliminary: nucleic acid sequence not shown;
            translation not shown
#molecule_type DNA
#residues  1-155 #label KUN
#experimental_source strain 168
GENETICS
#gene      ytaB
SUMMARY    #length 155 #molecular-weight 17288 #checksum 6944
            Query Match 13.7%; Score 160; DB 2; Length 155;
            Best Local Similarity 27.9%; Pred. No. 4.83e-08;
            Matches 34; Conservative 29; Mismatches 57; Indels 2; Gaps 2;

Db 31 WYNSLKKPDWTPSGTAIGIWAIFALISAAIVVAARS-FPKAKSFFTLLIN-YVLN 88
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 33 WYAGLQKPSHPHWPVWGLYSAMGYSLVWVKELGGFTKEKAVVPLGLYTGQLAN 92
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 89 QAFSYQFTQKNLLASDCLLVAVITALLIILAKKYSRAASVLLPLPLWLSAFATFLSF 148
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 93 WANPPIFFGARGWALVDLLLVSGRAAATVAVYQVSPLAARLLPYLANLAFATTLN 152
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 149 TI 150
    :
QY 153 CV 154

RESULT 13
#status    ##molecule_type DNA
            nucleic acid sequence not shown

```

```

ENTRY      S76477      #type complete
TITLE      hypothetical protein - Synecchocystis sp. (PCC 6803)
ORGANISM   Synecchocystis sp.
DATE       25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change
ACCESSIONS S76477
REFERENCE   S74322
#authors   Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.;
            Nakamura, Y.; Miyajima, N.; Hirose, M.; Sugita, M.;
            Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.;
            Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shampo,
            S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.;
            Yasuda, M.; Tabata, S.
#journal   DNA Res. (1996) 3:109-136
#title     Sequence analysis of the genome of the unicellular
            cyanobacterium Synecchocystis sp. PCC6803. II. Sequence
            determination of the entire genome and assignment of
            potential protein-coding regions.
#cross-references EMBL:D90915; NID:g1653604; PID:d1019339; PID:g1653694
            the nucleotide sequence was submitted to the EMBL Data
            Library, June 1996
#accession S76477
#status    nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues  1-159 #label KAN
#cross-references EMBL:D90915; NID:g1653604; PID:d1019339; PID:g1653694
            the nucleotide sequence was submitted to the EMBL Data
            Library, June 1996
GENETICS
#start_codon GTG
SUMMARY    #length 159 #molecular-weight 17809 #checksum 1905
            Query Match 11.1%; Score 130; DB 2; Length 159;
            Best Local Similarity 25.0%; Pred. No. 3.58e-04;
            Matches 30; Conservative 30; Mismatches 55; Indels 5; Gaps 3;

Db 29 LRFNRLRRPSWLTETWIAFPFTWIAIFATGATLANNATADPGHRMGLAVGYLLELT 88
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 31 LRWYAGLQKPSHPHWPVWGLYSAMGYSLVWVKELGGFTKEKAVVPLGLYTGQLA 90
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 89 VM-AATPVWCKLSRVSGIIGATGFFVGLALVIAVS--QVSTTAFGLVPELSPICGT 145
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 91 LNWANPPIFFGAR--QMGWALVDLLLVSGAAATTVAVYQVSPLAARLLPYLANLAFAT 148
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 14
ENTRY      S45776      #type complete
TITLE      uracil transport protein homolog YBL042c - yeast
            (Saccharomyces cerevisiae)
ALTERNATE_NAMES protein YBL0406
ORGANISM   Saccharomyces cerevisiae
DATE       26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change
ACCESSIONS S45776; S50783
REFERENCE   S45745
#authors   Goffeau, A.; Jonniaux, J.L.; Purnelle, B.; Skala, J.; de
            Wergifosse, P.; van Dyck, L.
#submission submitted to the Protein Sequence Database, August 1994
#accession S45776
#molecule_type DNA
#residues  1-639 #label GOF
#cross-references EMBL:Z35803; NID:g536058; PID:g536059; MIPS:YBL042c
            #experimental_source strain S288C
REFERENCE   S50284
#authors   de Wergifosse, P.; Jacques, B.; Jonniaux, J.L.; Purnelle, B.;
            Skala, J.; Goffeau, A.
#journal   Yeast (1994) 10:1489-1496
#title     The sequence of a 22.4 kb DNA fragment from the left arm of
            yeast chromosome II reveals homologues to bacterial proline
            synthetase and murine alpha-adaptin, as well as a new
            permease and a DNA-binding protein.
#accession S50783
#status    nucleic acid sequence not shown
            ##molecule_type DNA

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11

MPERCH_PP

***** (TM)

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MPerch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Jul 21 14:54:08 1998; MasPar time 6.91 Seconds
613.189 Million cell updates/sec
Tabular output not generated.

Title: >US-09-047-652A-3
Description: (1-169) from US09047652A.pep
Perfect Score: 1170
Sequence: 1 XXXXXXXXXXXXXXXXXXXXXXXX.....LNYCVRDNGWGRRLPE 169

Scoring table: PAM 150
Gap 11

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 43.233; Variance 89.342; scale 0.484

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	1160	99.1	169	1	PKBS_HUMAN PERIPHERAL-TYPE BENZODIAZEPINE RECOGNITION SITES AND IS MOST LIKELY TO COMPRISE BINDING DOMAINS FOR BENZODIAZEPINES AND ISOQUINOLINE CARBOXYAMIDES.	3.59e+203
2	1008	86.2	169	1	PKBS_MOUSE PERIPHERAL-TYPE BENZODIAZEPINE RECOGNITION SITES AND IS MOST LIKELY TO COMPRISE BINDING DOMAINS FOR BENZODIAZEPINES AND ISOQUINOLINE CARBOXYAMIDES.	1.94e+172
3	1000	85.5	169	1	PKBS_RAT PERIPHERAL-TYPE BENZODIAZEPINE RECOGNITION SITES AND IS MOST LIKELY TO COMPRISE BINDING DOMAINS FOR BENZODIAZEPINES AND ISOQUINOLINE CARBOXYAMIDES.	7.93e+171
4	944	80.7	169	1	PKBS_BOVIN PERIPHERAL-TYPE BENZODIAZEPINE RECOGNITION SITES AND IS MOST LIKELY TO COMPRISE BINDING DOMAINS FOR BENZODIAZEPINES AND ISOQUINOLINE CARBOXYAMIDES.	1.48e+159
5	339	29.0	169	1	CRTH_RHOCA CRTK PROTEIN.	3.11e+41
6	115	9.8	639	1	YBE2_YEAST PUTATIVE TRANSPORTER Y	2.22e+03
7	105	9.0	283	1	LEP3_ERWCH TYPE 4 PREPILIN-LIKE P	4.81e+02
8	101	8.6	246	1	GLTJ_ECOLI GLUTAMATE/ASPARTATE TR	1.58e+01
9	100	8.5	418	1	MHPT_ECOLI PUTATIVE 3-HYDROXYPHEN	2.11e+01
10	97	8.3	271	1	CDS4_PSEAE PHOSPHATIDATE CYTIDILY	5.01e+01
11	97	8.3	518	1	AMTG_BACS7 GLUCAN 1,4-ALPHA-MALTO	5.01e+01
12	95	8.1	447	1	FD3C_SCHPO OMEGA-3 FATTY ACID DES	8.83e+01
13	95	8.1	589	1	FUR4_SCHPO URACIL PERMEASE.	8.83e+01
14	94	8.0	759	1	SC11_YEAST CTRL1 SUPPRESSOR PROTEI	1.17e+00
15	92	7.9	213	1	IF4E_XENLA EUKARYOTIC TRANSLATION	2.03e+00
16	92	7.9	283	1	CCMC_BRAJA HEME EXPORTER PROTEIN	2.03e+00
17	93	7.9	453	1	FD3C_SOYBN OMEGA-3 FATTY ACID DES	1.54e+00
18	92	7.9	677	1	BETT_ECOLI HIGH-AFFINITY CHOLINE	2.03e+00
19	91	7.8	245	1	CCMC_ECOLI HEME EXPORTER PROTEIN	2.68e+00
20	91	7.8	438	1	FUMC_SULSO FUMARATE HYDRATASE CLA	2.68e+00
21	91	7.8	446	1	FD3C_ARATH OMEGA-3 FATTY ACID DES	2.68e+00
22	91	7.8	488	1	OSMA_ERWCH OSMOPROTECTANT UPTAKE	2.68e+00
23	90	7.7	434	1	YNM8_YEAST HYPOTHETICAL 50.2 KD P	3.51e+00

Query Match 99.1%; Score 1160; DB 1; Length 169;
Best Local Similarity 98.6%; Pred. No. 3.59e+203;

24	89	7.6	308	1	CYB_COIRU CYTOCHROME B (EC 1.10.	4.60e+00
25	89	7.6	317	1	QOX1_SULAC QUINOL OXIDASE POLYPEP	4.60e+00
26	88	7.5	318	1	LPLB_BACSU LPLB PROTEIN.	6.01e+00
27	88	7.5	381	1	OPS2_DROME OPSIN RH2 (CELLULAR OPS	6.01e+00
28	88	7.5	389	1	VMSA_HPBVM MAJOR SURFACE ANTIGEN	6.01e+00
29	88	7.5	400	1	VMSA_HPBV9 MAJOR SURFACE ANTIGEN	6.01e+00
30	88	7.5	400	1	VMSA_HPBV2 MAJOR SURFACE ANTIGEN	6.01e+00
31	88	7.5	859	1	OBP_HSVBC REPLICATION ORIGIN BIN	6.01e+00
32	88	7.5	2127	1	RRPL_RABVS RNA POLYMERASE BETA SU	6.01e+00
33	88	7.5	2142	1	RRPL_RABVS RNA POLYMERASE BETA SU	6.01e+00
34	87	7.4	196	1	VATL_DICDI VACUOLAR ATP SYNTHASE	7.83e+00
35	87	7.4	225	1	US07_HCMVA HYPOTHETICAL PROTEIN H	7.83e+00
36	87	7.4	226	1	VMSA_HPBVD MAJOR SURFACE ANTIGEN.	7.83e+00
37	87	7.4	226	1	VMSA_HPBVS MAJOR SURFACE ANTIGEN.	7.83e+00
38	87	7.4	400	1	VMSA_HPBVP MAJOR SURFACE ANTIGEN	7.83e+00
39	87	7.4	404	1	IDH1_VIBAL OMEGA-3 FATTY ACID DES	7.83e+00
40	87	7.4	414	1	IDH1_VIBAL ISOCITRATE DEHYDROGENA	7.83e+00
41	86	7.4	443	1	YZ06_MYCTU HYPOTHETICAL 43.6 KD P	1.02e+01
42	86	7.4	457	1	NUAM_ARBLI NADH-UBIQUINONE OXIDOR	1.02e+01
43	87	7.4	496	1	NANT_ECOLI PUTATIVE SIALIC ACID T	7.83e+00
44	87	7.4	753	1	PMT3_YEAST DOLICHYL-PHOSPHATE-MAN	7.83e+00
45	87	7.4	857	1	ENV_HV2KR ENVELOPE POLYPROTEIN G	7.83e+00

ALIGNMENTS

RESULT 1	PKBS_HUMAN	STANDARD;	PRT;	169 AA.
AC	P30536;			
DT	01-APR-1993 (REL. 25, CREATED)			
DT	01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)			
DT	01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)			
DE	PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (PBR) (PKBS) (MITOCHONDRIAL			
DE	BENZODIAZEPINE RECEPTOR).			
GN	BZRP OR MBR			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; PRIMATES.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 91146565.			
RA	RIOND J., MATTEI M.G., KAGHAD M., DUMONT X., GUILLEMOT J.C.,			
RA	LE FUR G., CAPUT D., FERRARA P.;			
RL	EUR. J. BIOCHEM. 195:305-311(1991).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 95237610.			
RA	YAKOVLEV A.G., RUFFO M., JURKA J., KRUEGER K.E.;			
RL	GENE 135:201-205(1995).			
CC	-1- FUNCTION: RESPONSIBLE FOR THE MANIFESTATION OF PERIPHERAL-TYPE			
CC	BENZODIAZEPINE RECOGNITION SITES AND IS MOST LIKELY TO COMPRISE			
CC	BINDING DOMAINS FOR BENZODIAZEPINES AND ISOQUINOLINE CARBOXYAMIDES.			
CC	MAY PLAY A ROLE IN THE TRANSPORT OF PORPHYRINS AND HEME.			
CC	-1- SUBCELLULAR LOCATION: MITOCHONDRION; INTEGRAL MEMBRANE PROTEIN.			
CC	-1- SIMILARITY: SEGMENTS TM1, TM4, AND TM5 SHOW SIMILARITY WITH THE			
CC	TRANSMEMBRANE SEGMENTS M1, M2, AND M4 FROM SUBUNITS OF THE			
CC	GABA(A)/BENZODIAZEPINE RECEPTOR FAMILY, RESPECTIVELY.			
DR	EMBL: M36035; G306883; -			
DR	EMBL: U12421; G529946; -			
DR	PIR: S14257; S14257.			
DR	MIM: 109610; -			
KW	MITOCHONDRION; RECEPTOR; TRANSMEMBRANE.			
FT	TRANSMEM 6 26 TM1 (POTENTIAL).			
FT	TRANSMEM 47 67 TM2 (POTENTIAL).			
FT	TRANSMEM 80 100 TM3 (POTENTIAL).			
FT	TRANSMEM 106 126 TM4 (POTENTIAL).			
FT	TRANSMEM 135 155 TM5 (POTENTIAL).			
FT	CONFLICT 147 147 A -> T (IN REF. 2).			
FT	CONFLICT 162 162 H -> R (IN REF. 2).			
SQ	SEQUENCE 169 AA; 18779 MW; EC07D06E CRC32;			

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[W][I][L][D][E][R][N][E][S][S]
[T][M]

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Jul 21 14:54:44 1998; MasPar time 12.32 Seconds
577.651 Million cell updates/sec
Tabular output not generated.

Title: >US-09-047-652A-3
Description: (1-169) from US09047652A.pep
Perfect Score: 1170
Sequence: 1 XXXXXXXXXXXXXXXXXXXXXXXX.....LNYCVRDNRHNGRRLPE 169

Scoring table: PAM 150
Gap 11

Searched: 140542 seqs, 42109429 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl5
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 42.037; Variance 94.668; scale 0.444

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	995	85.0	169	10	BENZODIAZEPINE RECEPTOR	4.27e-156
2	956	81.7	169	2	PERIPHERAL BENZODIAZEPINE	7.01e-149
3	327	27.9	153	9	MITOCHONDRIAL BENZODIAZEPINE	8.96e-36
4	291	24.9	157	9	CRT GENES	1.02e-29
5	245	20.9	553	3	HYPOTHETICAL PROTEIN C	3.72e-22
6	211	18.0	31	10	MITOCHONDRIAL BENZODIAZEPINE	9.88e-17
7	160	13.7	155	9	YTAB PROTEIN	5.49e-09
8	130	11.1	159	9	HYPOTHETICAL 17.8 KD P	9.21e-05
9	105	9.0	634	9	HYPOTHETICAL 69.4 KD P	1.55e-01
10	102	8.7	188	9	PUTATIVE GTG START COD	3.58e-01
11	102	8.7	285	9	HYPOTHETICAL 32.0 KD P	6.21e-01
12	100	8.5	292	9	YOAV	6.21e-01
13	100	8.5	368	5	MHC CLASS I PROTEIN PR	6.21e-01
14	99	8.5	380	8	PLASTID OMEGA-3 FATTY	8.16e-01
15	99	8.5	436	8	DELTA-15 LINEOYL DESAT	8.16e-01
16	100	8.5	537	9	HYPOTHETICAL 57.1 KD P	6.21e-01
17	98	8.4	209	9	HYPOTHETICAL 21.6 KD P	1.07e+00
18	97	8.3	372	9	HYPOTHETICAL 40.5 KD P	1.40e+00
19	97	8.3	438	8	OMEGA-3 FATTY ACID DES	1.40e+00
20	96	8.2	160	8	RNA POLYMERASE (FRAGME	1.83e+00

21	96	8.2	261	9	P94945	FWUG, FWUD AND FWUB GE	1.83e+00
22	96	8.2	354	3	O16444	C54F6.7 PROTEIN.	1.83e+00
23	95	8.1	321	9	P95137	HYPOTHETICAL 35.9 KD P	2.39e+00
24	95	8.1	398	8	O24626	FATTY ACID DESATURASE	2.39e+00
25	95	8.1	443	8	O33824	FATTY ACID DESATURASE	2.39e+00
26	95	8.1	637	9	O31688	YKVV PROTEIN.	2.39e+00
27	94	8.0	441	8	P93350	OMEGA-3 FATTY ACID DES	3.11e+00
28	94	8.0	581	1	O14035	HYPOTHETICAL 64.1 KD P	3.11e+00
29	93	7.9	535	9	O53111	CBB3-TYPE CYTOCHROME O	4.04e+00
30	92	7.9	676	2	O15296	15S-LIPOXYGENASE	5.24e+00
31	93	7.9	685	8	P93156	CELLULOSE SYNTHASE (FR	4.04e+00
32	92	7.9	700	9	O84660	SENSORY TRANSDUCTION H	5.34e+00
33	91	7.8	117	9	O32937	HYPOTHETICAL 12.4 KD P	6.78e+00
34	91	7.8	458	6	O21406	NADH DEHYDROGENASE SUB	6.78e+00
35	91	7.8	533	9	O51179	HYPOTHETICAL 57.1 KD P	6.78e+00
36	90	7.7	332	9	P73433	HYPOTHETICAL 36.6 KD P	8.76e+00
37	90	7.7	389	11	O67875	PRE S1/S ORF.	8.76e+00
38	90	7.7	432	9	P77540	BENZOATE MEMBRANE TRAN	8.76e+00
39	90	7.7	439	1	O13295	ALPHA-GALACTOSIDASE.	8.76e+00
40	90	7.7	478	9	P76103	FROM BASES 1496666 TO	8.76e+00
41	89	7.6	378	11	O67955	HBV SURFACE PROTEINS (1.13e+01
42	89	7.6	460	9	P77429	FROM BASES 1676082 TO	1.13e+01
43	89	7.6	461	3	P91197	SIMILAR TO LIGAND-GATE	1.13e+01
44	88	7.5	281	11	O41740	MIDDLE S PROTEIN.	1.45e+01
45	88	7.5	389	11	O67890	HBV SURFACE PROTEINS.	1.45e+01

ALIGNMENTS

RESULT 1
ID Q62118 PRELIMINARY; PRT; 169 AA.
AC Q62118;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE BENZODIAZEPINE RECEPTOR, PERIPHERAL (PERIPHERAL-TYPE BENZODIAZEPINE
DE RECEPTOR).
GN BZRP.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA TAKETANI S., KOHNO H., OKUDA M., FURUKAWA T., TOKUNAGA R.;
RL J. BIOL. CHEM. 269:2527-7531(1994).
DR EMBL; D21207; G484054; -;
DR MGD; MGI:88222; BZRP.
SQ SEQUENCE 169 AA; 18829 MW; 90CAC703 CRC32;

Query Match 85.0%; Score 995; DB 10; Length 169;
Best Local Similarity 83.2%; Pred. No. 4.27e-156;
Matches 119; Conservative 14; Mismatches 10; Indels 0; Gaps 0;
Db 27 RGEGLRWYASLQKPSWHPRTWLAPINATLYSANGYSYIWKELGFTEDAMVPLGLYT 86
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 27 HGEGLRWYAGLQKPSWHPRTWLAPINATLYSANGYSYIWKELGFTEDAMVPLGLYT 86
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 87 GQLALNANWPPFFGARGQMGWALADLLVSCVATATTLAWHRVSPPARLLPYLAWLAF 146
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 87 GQLALNANWPPFFGARGQMGWALADLLVSCVATATTLAWHRVSPPARLLPYLAWLAF 146
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 147 ATVLNYYVRDNRSGRGGSLRAE 169
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 147 TTTLYCVRDNRHNGRRLPE 169
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
RESULT 2
ID Q13850 PRELIMINARY; PRT; 169 AA.
AC Q13850;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)

DE PERIPHERAL BENZODIAZEPINE RECEPTOR.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
[1]

RP SEQUENCE FROM N.A.
RC TISSUE-PLACENTA;
RX MEDLINE; 94140364.
RA LIN D., CHANG Y.J., STRAUSS J.F., MILLER W.L.;
RL GENOMICS 18:643-650(1993).
DR EMBL; L21954; G488425; -.
DR EMBL; L21952; G488425; JOINED.
DR EMBL; L21953; G488425; JOINED.
SQ SEQUENCE 169 AA; 18483 MW; E528DC71 CRC32;

Query Match 81.7%; Score 956; DB 2; Length 169;
Best Local Similarity 86.2%; Pred. No. 7,01e-149;
Matches 125; Conservative 7; Mismatches 9; Indels 4; Gaps 4;

Db 27 HGEGLRWYAGLQKPSWHPHVLGPGVMTGLYSAMGYSLYKWLKELGFTKAVGSPGLH 86
Qy 27 HGEGLRWYAGLQKPSWHPHVLGPGVMTGLYSAMGYSLYKWLKELGFTKAVVPLG-LY 85
Db 87 WAAGPELGM-A-PHLL-GARQMGWALVDLLLVSGAAATTVAVYQVSPLAARLLPYLAWL 144
Qy 86 -TGQALNMAWPPPIFFGARQMGWALVDLLLVSGAAATTVAVYQVSPLAARLLPYLAWL 144
Db 145 AFATTLNVCVVRDNGHGGRRRLPE 169
Qy 145 AFTTLNVCVVRDNGHGGRRRLPE 169

RESULT 3
ID O28797
AC O28797;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE MITOCHONDRIAL BENZODIAZEPINE RECEPTOR/SENSORY TRANSDUCTION PROTEIN.
GN AF1475.
OS ARCHAEOLLOBUS FULGIDUS.
OC ARCHAEABACTERIA; EURYARCHAEOTA; ARCHAEOLLOBALES; ARCHAEOLLOBACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RA KLENK H.P., CLAYTON R.A., TOMB J., WHITE O., NELSON K.E.,
RA KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,
RA RICHARDSON D.L., KERLAVAGE A.R., GRAHAM D.E., KYRIDES N.C.,
RA FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,
RA KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.,
RA PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOU L.,
RA OVERBECK R., GOCAYNE J.D., WEIDMAN J.F., McDONALD L., UTTERBACK T.,
RA COTTON M.D., SPRIGGS T., ARTTACH P., KAINE B.P., SYKES S.M.,
RA SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,
RA MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESSE C.R.,
RA VENTER J.C.;
RL SUBMITTED (DEC-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
[2]
RP SEQUENCE FROM N.A.
RA KLENK H.P., CLAYTON R.A., TOMB J., WHITE O., NELSON K.E.,
RA KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,
RA RICHARDSON D.L., KERLAVAGE A.R., GRAHAM D.E., KYRIDES N.C.,
RA FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,
RA KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.,
RA PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOU L.,
RA OVERBECK R., GOCAYNE J.D., WEIDMAN J.F., McDONALD L., UTTERBACK T.,
RA COTTON M.D., SPRIGGS T., ARTTACH P., KAINE B.P., SYKES S.M.,
RA SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,
RA MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESSE C.R.,
RA VENTER J.C.;
RL SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; AE001001; G2649094; -.
SQ SEQUENCE 133 AA; 17185 MW; F7796417 CRC32;

Query Match 27.9%; Score 327; DB 9; Length 153;
Best Local Similarity 39.0%; Pred. No. 8.96e-36;
Matches 48; Conservative 30; Mismatches 39; Indels 6; Gaps 6;
Db 31 WYAGVEKPPFPNWLFGPANTLLYFLIGIVLYIAN-E-NGFWNDSRVKATFTT-QLGLN 87
Qy 33 WYAGLQKPSWHPHVLGPGVMTGLYSAMGYSLYKWLKELGFTKAVVPLGLYTGQALN 92
Db 88 FLWSILFFGLQNLPA-GLVDIIADIAVITIVYVHHSK-ASLLLPYLGLWILFASALN 145
Qy 93 WANPPIFFGARQ-MGWALVDLLLVSGAAATTVAVYQVSPLAARLLPYLAWLAFITTLN 151
Db 146 FAI 148
Qy 152 YCV 154

RESULT 4
ID Q54791
AC Q54791;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE CRT GENES.
GN CRTK.
OS RHODOBACTER SPHAEROIDES (RHODOSEUDOMONAS SPHAEROIDES).
OC PROKARYOTA; GRACILICUTES; ANOXYPHOTOBACTERIA; PURPLE BACTERIA;
OC RHODOSPIRILLACEAE.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NCIB 8253;
RX MEDLINE; 95238278.
RA LANG H.P., COGDELL R.J., TAKAICHI S., HUNTER C.N.;
RL J. BACTERIOL. 177:2064-2073(1995).
DR EMBL; X82458; G575409; -
SQ SEQUENCE 157 AA; 17854 MW; D56D5781 CRC32;

Query Match 24.9%; Score 291; DB 9; Length 157;
Best Local Similarity 36.7%; Pred. No. 1.02e-29;
Matches 44; Conservative 28; Mismatches 42; Indels 6; Gaps 5;

Db 30 WYDNLKFPWNPFRVFPPLAWTSLYFLMSLAPC-GWR--SS-KVRAGAGL-LCA-QLAFN 83
Qy 33 WYAGLQKPSWHPHVLGPGVMTGLYSAMGYSLYKWLKELGFTKAVVPLGLYTGQALN 92
Db 84 TLWTPVFFGKRMATALAVVWMLFVAATWMAFFOLDTWAGLVFVPLIWAATAATGLNF 143
Qy 93 WANPPIFFGARQMGWALVDLLLVSGAAATTVAVYQVSPLAARLLPYLAWLAFITTLN 152

RESULT 5
ID Q93367
AC Q93367;
DT 01-FEB-1997 (TREMBLREL. 02, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL PROTEIN C41G7.3.
GN C41G7.3.
OS CAENORHABDITIS ELEGANS.
OC EUKARYOTA; METAZOA; ACCELLOMATES; NEMATODA; SECERNENTEA; RHABDITIDA.
RN [1]
RP SEQUENCE FROM N.A.
RA STEWARD C.;
RL SUBMITTED (OCT-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94150718.
RA WILSON R., AINSOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J.,
RA COULSON A., CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A.,
RA FULTON L., GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M.,
RA JOHNSTON L., JONES M., KERSHAW J., KIRSTEN J., LAISTER N.,
RA LAITREILLE P., LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B.,

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RA BROUILLET S., BRUSCHI C.V., CALDWELL B., CAPUANO V., CARTER N.M.,
RA CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A.,
RA DENIZOT F., DEVINE K.M., DUSTERHOF A., EHRLICH S.D., ENMERSON P.T.,
RA ENTIAN K.D., ERRINGTON J., FABRET C., FERRARI E., FOULGER D.,
RA FRITZ C., FUJITA M., FUJITA Y., FUMA S., GALIZZI A., GALLERON N.,
RA GHIM S.T., GLASER P., GOFFEAU A., GOLIGHTLY E.J., GRANDI G.,
RA GUISEPPI G., GUY B.J., HAGA K., HAIECH J., HARWOOD C.R., HENAUT A.,
RA HILBERT H., HOLSAPPEL S., HOSONO S., HULLO M.F., ITAYA M., JONES L.,
RA JORIS B., KARAYATA D., KASAHARA Y., KLAERR-BLANCHARD M., KLEIN C.,
RA KOBAYASHI Y., KOETTER P., KONINGSSTEIN G., KROGH S., KUMANO M.,
RA KURITA K., LAPIDUS A., LARINOIS S., LAUBER J., LAZAREVIC V.,
RA LEE S.M., LEVINE A., LIU H., MASUDA S., MAUEL C., MEDIGUE C.,
RA MEDINA N., MELLADO R.P., MIZUNO M., MOESTL D., NAKAI S., NOBACK M.,
RA NOONE D., O'REILLY M., OGAWA K., OGIWARA A., OUDEGA B., PARK S.H.,
RA PARRO V., POHL T.M., PORTELELE D., PORMOLLIK S., PRESCOTT A.M.,
RA PRESCAN E., PUJIC P., PURNELLE B., RAPOPORT G., REY M., REYNOLDS S.,
RA RIEGER M., RIVOLTA C., ROCHA E., ROCHE B., ROSE M., SADAIE Y.,
RA SATO T., SCANLAN E., SCHLEICH S., SCHROETER R., SCOFFONE F.,
RA SEKIGUCHI J., SEKOWSKA A., SEROT S.J., SERROR P., SHIN B.S., SOLDI B.,
RA SOROKIN A., TACCONI E., TAKAGI T., TAKAHASHI H., TAKEMARU K.,
RA TAKEUCHI M., TAMAKOSHI A., TANAKA T., TERPSTRA P., TOGNONI A.,
RA TOSATO V., UCHIYAMA S., VANDENBOL M., VANNIER F., VASSAROTTI A.,
RA VIARI A., WAMBUIT R., WEDLER E., WEDLER H., WEITZENEGER T.,
RA WINTERS P., WIPAT A., YAMAMOTO H., YAMANE K., YASUMOTO K., YATA K.,
RA YOSHIDA K., YOSHIKAWA H.F., ZUNSTEIN E., YOSHIKAWA H., DANCHIN A.,
RA NATURE 390:249-256(1997).
RL [2]
RP SEQUENCE FROM N.A.
RC STRAIN-168;
RA KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
RL SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
RL [3]
RP SEQUENCE OF 119-155 FROM N.A.
RX MEDLINE; 94195107.
RA KIEL J.A., BOELS J.M., BELOMAN G., VENEMA G.;
RL MOL. MICROBIOL. 11:203-218(1994).
RL [4]
RP SEQUENCE FROM N.A.
RA LAPIDUS A., GALLERON N., SOROKIN A., EHRLICH D.;
RP SUBMITTED (JUN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR EMBL; Z39119; E1185966;
DR EMBL; AF008220; G2293285;
SQ SEQUENCE 155 AA; 17288 MW; 875DAD85 CRC32;

Query Match 13.7%; Score 160; DB 9; Length 155;
Best Local Similarity 27.9%; Pred. No. 5,49e-09;
Matches 34; Conservative 29; Mismatches 57; Indels 2; Gaps

Db 31 WYNSKKPDPWTPSGTAIGIWIWAILFALISLSAAIYVAAFS-FKGAKSFWFTLLIN-YVLN 88
QY 33 WYAGLKQSPWHPHWLGPWVGTLYSAGVSYLWKELGGTERAVVPLGTYTQALN 92
Db 89 QAFSYQFTQKNLLAASDCLLIVATVILLIIAKKYSAASYLLPLPFLMSAFATFLSF 148
QY 93 WAWPPPIFFGARQMGWALVDLLVLSVAAAATVAVYQVSPLAARLLYPYLAWLAFTTLLN 152
Db 149 TI 150
QY 153 CV 154

RESULT 8
ID P74502 PRELIMINARY; PRT; 159 AA.
AC P74502;
DT 01-FEB-1997 (TREMBLREL. 02, CREATED)
DT 01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)
DE 01-FEB-1997 (TREMBLREL. 02, LAST ANNOTATION UPDATE)
DT HYPOTHETICAL 17.8 KD PROTEIN.
OS SYNECHOCYSTIS SP.
OC EUBACTERIA; CYANOBACTERIA; CHROCOCCOCALES; SYNECHOCYSTIS.
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN-PCC5803;

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[illegible]

Db 293 GL-QEPLTLRWEPPQTSFLTSSMG-IIVGLVLLVMVAVVAAAIV 335

	Query Match	8.5%	Score 99:	DB 8:	Length 436;
	Best Local Similarity	36.7%	Pred. No. 8.16e-01;		
	Matches 18;	Conservative	11;	Mismatches 14;	Indels 6; Gaps 6
Db	107	WRSMS - YVVRDVIIVLGLAAVAANSWAVNP - LYVVAQCTMEFWALFVL	153		
Qy	68	WKELGGETEKAVV - PLGLYITGQLALN-WA-WPPIFFFGAR-QMGWALVDL	112		

Search completed: Tue Jul 21 14:55:36 1998
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